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Sequence 43, Appl
Sequence 43, Appl
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Sequence 3114, A
Sequence 31114, A
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38, Appl
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375, Appli
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US-09-764-325A-23
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US-09-912-935-23
US-09-913-055-2
US-09-945-065-2
US-09-945-065-2
US-09-943-061-2
US-09-345-294-28
US-08-313-634-28
US-08-313-634-38
US-08-318-534-28
US-08-318-534-28
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US-09-252-991A-31114
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                 GenCore version (c) 1993 - 2005
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Perfect :
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28 88 4.0 606 3 US-09-041-236-4 Sequence 4, Appli 29 88 4.0 606 4 US-09-771-467C-4 Sequence 4, Appli 30 87.5 3.9 1969 3 US-08-816-22-16 Sequence 16, Appli 31 87.5 3.9 1969 3 US-08-816-228-16 Sequence 16, Appli 32 86.5 3.9 1969 109-252-991A-31349 Sequence 16, Appli 32 86.5 3.9 577 4 US-09-4816-248-17 Sequence 1373, A 35 85.5 3.9 284 2 US-08-826-939-2 Sequence 2, Appli 36 85.5 3.9 284 2 US-08-826-939-2 Sequence 2, Appli 36 85.5 3.9 284 2 US-08-826-939-2 Sequence 2, Appli 38 85.5 3.9 284 2 US-08-826-439-2 Sequence 2, Appli 39 85.5 3.9 284 2 US-08-826-439-2 Sequence 2, Appli 39 85.5 3.9 284 2 US-08-826-439-2 Sequence 2, Appli 41 84.5 3.8 490 4 US-09-461-225-250 Sequence 250, Appli 42 84.5 3.8 490 4 US-10-125-518 Sequence 250, Appli 44 84.5 3.8 490 4 US-10-12-54-250 Sequence 250, Appli 44 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 518, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-10-115-123-518 Sequence 250, Appli 56 84.5 3.8 490 4 US-1
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## ALIGNMENTS

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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE FILE OF INVENTION: POLYPEPTIDES AND POLYNUCLECTIDES
FILE REPERBYCE: 32066/37483
CURRENT PAPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR PILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PALCHIN Version 3.0
SEQ ID NO 36
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Pred. No. 1.7e-168;
0; Mismatches 7; Indels 1.
US-09-912-935-36
; Sequence 36, Application US/09912935
; Patent No. 6673904
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80.9%;
94.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 343; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
COGANISM: Homo sapiens
US-09-912-935-36
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STEM CELL GROWTH FACTOR-LIKE
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                                                                                                      DB 4; Length 529;
                                                                                                                                       Indels
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TILLE OF INVENTION: METHODS AND MATERIALS RELATING TO STER.
TITLE OF INVENTION: DOLYPEPTIDES AND POLYNUCLEOTIDES
TILLE REPERENCE: 32066/37483
CURRENY APPLICATION NUMBER: US/09/912,935
CURRENY APPLICATION NUMBER: 2001-07/24
PRIOR APPLICATION NUMBER: PC7/US00/35260
PRIOR PILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN VETRION 3.0
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  48.1%; Score 1066.5; DB 4; 56.5%; Pred. No. 1.9e-96; ative 63; Mismatches 88;
                                                                                                                                         88;
                                                                                                   Query Match

48.1%; Score 1066.5; DB

Best Local Similarity 56.5%; Pred. No. 1.9e-96;

Matches 205; Conservative 63; Mismatches 88
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; SEQ ID NO 28
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-912-935-28
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ORGANISM: Homo
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                                                                                                                                     GENERAL INCORMATION:

APPLICANT: NISHIKAWA, MITSUO ET al.

APPLICANT: NISHIKAWA, MITSUO ET al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 28, Application US/09912935

Patent No. 6673904

GENERAL INFORMATION:
GENERAL INCORMATION:
GENERAL INCORMATION:
MITEUR OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPRESENCE: 32066/37483

CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT FILING DATE: 2001-07-24

PRIOR APPLICATION NUMBER: PCT/US00/35260

PRIOR PELICATION NUMBER: PCT/US00/35260

RIOR FILING DATE: 2000-12-23

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn version 3.0
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                                                                                                      Sequence 31, Application US/09912935 Patent No. 6673904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
US-09-912-935-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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LGTI 358
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US-09-912-935-28
                                                                        RESULT 2
US-09-912-935-31
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Patent No. 6673904
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: METHODS AND POLYNUCLEOTIDES
TITLE OF INVENTION:
FILE REFERENCE: 32066/33483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT APPLICATION NUMBER: PCT/US00/35260
PRIOR PILING DATE: 2000-12-23
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Patent No. 6673904
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLECTIDES
TITLE OF INVENTION:
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR PELICATION NUMBER: PCT/US00/35260
PRIOR PILING DATE: 2000-12-23
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47.2%; Score 1047.5; DB 4; Length 4
Best Local Similarity 56.9%; Pred. No. 1e-94;
Matches 203; Conservative 55; Mismatches 88; Indels
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SEQ ID NO 38
LENGTH: 530
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SOFTWARE: Patentin versi
SEQ ID NO 35
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US-09-912-935-35
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US-09-912-935-38
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Best Local Simil
Matches 203; C
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US-09-912-935-38
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TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERBNCE: 32066/37483
CURRENT FILIANG DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/USO0/35260
PRIOR PILING DATE: 2000-12-23
NUMBER: OF SEQ ID NOS: 53
SOFTWARE: PATENTIN Version 3.0
SEQ ID NO 34
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GPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDWVDSGCPEESKEKMCENTEPVETSSRTTT 394
                                                                                                                                                                                                                   T--SPSPYDGDLTTTS---SSLFIDSLTTEDDTKLNPYAGGDGLQ-NNLSPKTKGTPVHL 407
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                                                             PVKTGLSDAFM1LNPSPDVPESRRRS1FEYHR1ELDPSKVTSMSAVEFTPLPTCLQHRSC
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US-09-912-935-35
; Sequence 35, Application US/09912935
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ORGANISM: Homo sapiens
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patent No. 6667391

GENERAL INFORMATION:

APPLICANT: Labat, Ivan

APPLICANT: Labat, Ivan

APPLICANT: Labat, Ivan

APPLICANT: Tang, Y. T.

APPLICANT: Tang, Y. T.

APPLICANT: Tang, Y. T.

APPLICANT: Chao, Cheng-Chi

APPLICANT: Chao, Cheng-Chi

APPLICANT: Chao, Cheng-Chi

APPLICANT: Mize, Nancy K.

APPLICANT: Chao, Cheng-Chi

TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell

TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell

TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell

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TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell

FILE REFERENCE: 30266/37630A

CURRENT APPLICATION NUMBER: 09/547,358

PRIOR PELING DATE: 2000-04-11

PRIOR PELING DATE: 2000-04-01

SPEQ ID NO 25

LENGTH: 392

LENGTH: 392

LENGTH: 392

LENGTH: 392

LENGTH: 392
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                                                                                                                                         CEDFQDEDHDSASPDT--SFSPYDGDLTTTS---SSLFIDSLTTEDDTKLNPYAGGDGLQ 393
                                                        183 VEMTPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDWVDSGCPEESKERM
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42.7%; Score 948; DB 4; Length 392;
Best Local Similarity 57.9%; Pred. No. 6e-85;
Matches 184; Conservative 51; Mismatches 77; Indels
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US-09-764-325A-25
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GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Tang, Y. T.
APPLICANT: Tang, Y. T.
APPLICANT: Mize, Nancy K.
APPLICANT: Mize, Nancy K.
TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
TITLE OF INVENTION: MOMBER: US/09/764,325A
CURRENT PELICATION NUMBER: 09/547,358
FRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-07
SPRIOR FILING DATE: 2000-04-07
SPRIOR FILING DATE: 2000-04-07
SPRIOR FILING DATE: 2000-01-21
SPRIOR PRIOR PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FTFOAALHHDGRIVFAYKEIPMSVPEISSSOHPVKTGLSDAFMILNPSPDVPESRRRSIF 261
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57.9%; Pred. No. 6e-85;
ive 51; Mismatches 77; Indels
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-hem 77; Indels
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ORGANISM: Homo sapiens
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63 APLMANFDPSVSRNSTVRYFDNGTALVVQMDHVHLQDNYNLGSFTFQATLLMDGRIIFGY 122
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                                                                                                                                                                                                                                                                                                                                                                                  279 VEFTPLPTCLOHRSCDACMSSDLTFNCSWCHVLORCSSGFDRYROEWMDYGCAQEAEGRM 338
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                                                                                                                                                                                                   159 APLMANFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAY
                                                                99 RSQVKIHTILSNTHRQASRVVLSPDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYV
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APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING DATE: October 26, 1998
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Melanie K. Spriggs, Michael R. Comeau, APPLICANT: Robert F. DuBose, Richard S. Johnson TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: October 28, 1998
CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/958,598 (converted to APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PatentIn Release #1.0, Version #1.30
51; Mismatches
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October 28, 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 -NNLSPKTKGTPVHLGTI 410
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REGISTATION NUMBER: 245
REFERENCE/DOCKET NUMBER: 265
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Janis C. Henry STREET: 51 University St.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
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Matches 184; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
SOFTWARE: PatentI
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COUNTRY:
ZIP: 9810
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                                                                                                                         GENERAL INFORMATION:

APPLICANT: Nishikawa, Mitsuo et al.

APPLICANT: Nishikawa, Mitsuo et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483

CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT FILING DATE: 2001-07-24

PRIOR APPLICATION NUMBER: PCT/US00/35260

PRIOR FILING DATE: 2000-12-23
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APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 APLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQATLLMDGRIIFGY 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRM 338
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Pred. No. 6e-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.7%; Score 948; DB 4; Length 39
57.9%; Pred. No. 6e-85;
tive 51; Mismatches 77; Indels
                                                 Sequence 23, Application US/09912935
Patent No. 6673904
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Patent No. 6673904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 -NNLSPKTKGTPVHLGTI 410
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; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 23

; LENGTH: 392

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-912-935-23
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57.9%;
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SOFWARE: PatentIn version 3.0
SEQ ID NO 25
LENGTH: 392
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CRGANISM: Homo sapiens
US-09-912-935-25
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Best Local Similarity
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                        -09-912-935-23
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US-09-912-935-25
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                                                                                                                                                                                                                                             137;
                                                                                                                                                                                                    DB 3; Length 1568;
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Patent No. 6187909
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCES: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                  5.2%; Score 115.5; DB 3;
20.6%; Pred. No. 0.074;
tive 42; Mismatches 118;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS/Windows 95
                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1569 amino acids
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
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ATTORNBY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
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                                                                      TYPE: amino acid
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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hes 77; Conserv
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CITY: Seattle
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COUNTRY: US
ZIP: 98101
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US-09-459-066-2
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                                                                                                                                                                                                                                               256 GAATGWPSMAR----IAQSTEVLFQGQASLDCGHGH-----PDGR------R
                                                                                                                                                             Gaps
                                                                                                                                                           42; Mismatches 118; Indels 137;
                                                                                                                  Length 1568;
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Patent No. 6174689
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
                                                                                                             DB 3;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/458,791
FILING DATE: 10-Dec-1999
CLASSIFICATION: CURKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                             Query Match 5.2%; Score 115.5; DB Best Local Similarity 20.6%; Pred. No. 0.074;
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CORRESPONDENCE ADDRESS:
ADDRESSES: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
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516 KEKTTVTMVGSFSP 529
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COMPUTER READABLE FORM:
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                                                                                                                                                         77; Conservative
                                         / MOLECULE TYPE: protein US-09-181-706-2
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US-09-458-791-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----DFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVY 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22 GTVRGWNRRARESPGHVSEPDRT----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVS
                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                Indels 137;
                                                                                                                                                                                                                                        DB 3; Length 1568;
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APPLICANT: Spriggs, Melanie
APPLICANT: Spriggs, VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
                                                                                                                                                                                                                                        5.2%; Score 115.5; DB 3; 20.6%; Pred. No. 0.074; iive 42; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE:
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Patent No. 6562949
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                  TELECOMMUNICATION INFORMATION: TELEPHONE: (206)470-4189
                                                      TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
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REFERENCE/DOCKET NUMBER:
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Best Local Similarity 20.6;
Matches 77; Conservative
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MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. F
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256 GAATGWPSMAR----IAQSTEVLFQGQASLDCGHGH-----PDGR------R 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVVM------NRTVLF 391
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                                                                                                                                                                                                                                                                                                          Length 1568;
                                                                                                                                                                                                                                                                                                      Score 115.5; DB 4;
Pred. No. 0.074;
                                                                                                                                                                                                                                                                                                                                                 42; Mismatches 118;
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                   NAME: Henry, Janis C
REGISTRATION NUMBERS: 34,347
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION: INFORMATION:
                                                                                                                                  INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 1568 amino acids
                                                                                                                                                                                                                                                                                                        n 5.2%;
Similarity 20.6%;
                                                                                                TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 
Local 77; Conservative
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-459-065-2
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(c) 1993 - 2005 Compugen Ltd
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Listing first 45 summaries
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Sequence 36, Application US/09912935
Patent No. 6673904
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: DOLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: DOLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: DOLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION NUMBER: US/09/912,935
CURRENT APPLICATION NUMBER: PCT/US00/35260
PRIOR PILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
NUMBER OF SEQ ID NOS: 53
SEQ ID NO 36
SEQ ID NO 36
SEQ ID NO 36
SEQ ID NO 36
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; Sequence 38, Application US/09912935
; Patent No. 6673904
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE;
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: PCT/US00/35260
; PRIOR FILING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 38
                                                                                    Sequence 130, App
Sequence 131, App
Sequence 15, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 30, Appl
Sequence 38436, A
Sequence 53653, A
                                                                                                                                                                                                                                            Sequence 53653, A Sequence 191, App Sequence 6708, App Sequence 17517, A Sequence 16, Appl Sequence 16, Appl Sequence 14, Appl
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US-09-358-0558-137
US-09-383-238-17
US-09-283-238-17
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US-09-270-767-38436
US-09-270-388-191
US-09-270-388-191
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US-09-513-999C-6708
US-09-513-999C-6708
US-09-513-999C-6708
US-09-854-845-16
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ORGANISM: Homo sapiens
US-09-912-935-36
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Growth Factor-Like Polypeptides and Polynucleotides
               FILE REFERENCE: 30266/37630A
CURRENT APPLICATION NUMBER: US/09/764,325A
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 09/547,358
PRIOR PILING DATE: 2000-04-11
PRIOR PILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/545,714
PRIOR PILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VUMBER: 09/488,725
PRIOR PILING DATE: 2000-01-21
SOFTWARE: PATENTIN VUMBER: 09/488,725
FRIOR PILING DATE: 2000-01-21
SOFTWARE: PATENTIN VUMBER: 09/488,725
FRIOR PILING DATE: 2000-01-21
SOFTWARE: PATENTIN VOIC: 2.1
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Best Local Similarity 67.7%;
Matches 44; Conservative
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ORGANISM: Homo sapiens
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US-09-912-935-23
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227 ODWVD 231
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APPLICANT: Labat, Ivan
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
APPLICANT: Tang, Y. T.
APPLICANT: Tang, Y. T.
APPLICANT: Alze, Nancy K.
APPLICANT: Childs, John
TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polymucleotides
FILE REPERENCE: 30266/37630A
CURRENT APPLICATION NUMBER: 09/947,358
FILE REPEACATION NUMBER: 09/547,358
PRIOR FILING DATE: 2000-04-11
SPRIOR FILING DATE: 2000-04-11
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US-09-764-125A-25

Sequence 25, Application US/09764325A

Patent No. 6667391

GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Tang, Y. T.
APPLICANT: Tang, Y. T.
APPLICANT: Mize, Chang-Chi
APPLICANT: Mize, Nancy K.
APPLICANT: Mize, Nancy K.
APPLICANT: Childs, John
TITLE OF INVENTION: Methods and Materials Relating to No. 6667391e1 Stem Cell
                                                                                                                                                                                                                                                                                          304 YHRVELQMSKITNISAVEMTPLPTCLQFNGCGPCVSSQIGFNCSWCSKLQRCSSGFDRHR 363
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                                                                                                                                    Length 530;
                                                                                                                                                                                                   12; Indels
                                                                                                                                    Score 264; DB 4;
Pred. No. 1.2e-24;
9; Mismatches 12;
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                                                                                                                                          71.48;
67.78;
                                                                                                                                          Query Match
Best Local Similarity 67.7
Matches 44; Conservative
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CORGANISM: Homo sapiens
US-09-764-325A-23
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364 QDWVD 368
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227 QDWVD 231
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                     ; TYPE: PRT
; ORGANISM: Mouse
US-09-912-935-38
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US-09-764-325A-23
   LENGTH: 530
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patent No. 667304

GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
APPLICANTON: POLYPEPTIDES AND POLYNUCLEOTIDES
ATITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
ATITLE APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR PLING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SEQ ID NO 23
LENGTH: 392
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Patent No. 6673904
; GENERAL INPORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE;
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLECTIDES
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Score 263; DB 4; Length 392;
Pred. No. 1.1e-24;
9; Mismatches 12; Indels
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APPLICATION MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
GURRENT ELING DATE: 2006/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2000-107-24
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFFWARE: Patentin version 3.0
SEQ ID NO 31
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Patent No. 6673904
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION UNMERR: US/09/912,935
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR PRIOR DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                      Length 449;
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Pred. No. 1.3e-24;
9; Mismatches 12.
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                 SOFTWARE: Patentin version 3.0
SEQ ID NO 34
LENGTH: 449
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Best Local Similarity 67.7%;
Matches 44; Conservative
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Matches 44; Conservative
NUMBER OF SEQ ID NOS: 53
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                                                                                                      ; ORGANISM: Homo sapiens
US-09-912-935-34
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364 QDWVD 368
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SEQ ID NO 28
LENGTH: 529
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                                                                                    TYPE: PRT
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APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: \u00b109/0912,935
CURRENT PILLING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOPTWARE: PATCHIN Version 3.0
SEQ ID NO 35
LENGTH: 425
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Sequence 34, Application US/09912935
Patent NO. 6673904
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR PILING DATE: 2000-12-23
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Pred. No. 1.3e-24;
9; Mismatches 12; Indels
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             CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR PILING DATE: 2001-07-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn Version 3.0
SEQ ID NO 25
LENGTH: 392
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71.1%;
Best Local Similarity 67.7%;
Matches 44; Conservative
FILE REFERENCE: 32066/37483
                                                                                                                                                                                                                                                                                                                     44; Conservative
                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-912-935-35
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262 QDWVD 266
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227 QDWVD 231
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US-09-912-935-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Indels 10; Gaps
                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/958,598 (converted to a APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION:
PRIOR APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: --to be assigned-- (COSN 08/958,598)
FILING DATE: October 26, 1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 27.3%; Score 101; DB 3; Length 1568; Best Local Similarity 29.7%; Pred. No. 0.00079; Matches 22; Conservative 15; Mismatches 27; Indels 10
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US-09-458-791-2
; Sequence 2, Application US/09458791
; Patent No. 6174689
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
COMPATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILLING DATE: 10-Dec-1999
CLASSIFICATION: cUnknown>
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PAPPLICATION UNMERR: 08/958,598
FILLING DATE: 28-0CT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHAPACTERISTICS:
LENGTH: 1568 amino acids
TYPE: amino acid
  US/09/181,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSES: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
                        October 28, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98101
COMPUTER READABLE FORM:
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  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT PILING DATE: 2000-12-24
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOPTWARE: Patentin version 3.0
SEQ ID NO 40
LENGTH: 529
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                                                                                                                                                                                               304 YHRVELQMSKITHISAVEMTPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHR 363
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71.1%; Score 263; DB 4; Length 529;
l Similarity 67.7%; Pred. No. 1.6e-24;
44; Conservative 9; Mismatches 12; Indels
                                                                     Query Match 71.1%; Score 263; DB 4; Length 529; Best Local Similarity 67.7%; Pred. No. 1.6e-24; Matches 44; Conservative 9; Mismatches 12; Indels
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Patent No. 6130068

GENERAL INFORMATION:

APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Robert F. DuBose Richard S. Johnson

TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 40, Application US/09912935
Patent No. 6673904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-912-935-28
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Matches 44; Conserv
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364 QDWVD 368
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364 QDWVD 368
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STATE: WA
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                                                                                                                                                                                                                                                Query Match 27.3%; Score 101; DB 3; Length 1568; Best Local Similarity 29.7%; Pred. No. 0.00079; Matches 22; Conservative 15; Mismatches 27; Indels 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESONDENCE ADDRESS:
ADDRESSE: Janis C. Henry
STREET: 51 University St.
CITY: Seatle
STATE: WA
COUNTRY: US
ZIP: 99101
                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-458-791-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
                                                                                                  LENGTH: 1569 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
TELECOMMUNICATION INFORMATION
                   TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09459066
Patent No. 6187909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REPERENCE/DOCKET NUMBER: 265
TELECOMMUNICATION: INFORMATION:
TELEPHONE: (206)470-4189
                                                           INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  485 GDCVHSENLENWLD 498
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LENGTH: 1568 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-09-459-066-2
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MEDIUM TYPE: Floppy
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426 FYKLVPDPVKNIYIYLTAGKEVRRIRVANCNKHKSCSECLTA-TDPHCGWCHSLQRCTFQ 484
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                                                                                                                                                                                                                      | Sequence 2, Application US/09459065
| Patent No. 6562949
| GENERAL INFORMATION:
| APPLICANT: Spridgs, Melanie
| TITLE OF INVENTION: RECEPTOR DNA AND POLYBEPTIDES
| UNMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Sl University St.
| STREET: Sl University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: January 28, 2005, 22:14:14 Job time : 6.53163 secs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
TELECOMMUNICATION INFORMATION:
                                                                                                        485 GDCVHSENLENWLD 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206)470-4189
TELEFAX. (206)233-0644
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 aning acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: WA COUNTRY: U
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27; Indels 10;

Matches

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2005
          Copyright
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OM protein - protein search, using sw model Run on:

January 28, 2005, 21:52:02 ; Search time 130.231 Seconds (without alignments) 1129.372 Million cell updates/sec

US-09-918-715-230\_COPY\_18\_427 2218 Title: Perfect score:

1 ALSPQPGAGHDEGPGSGWAA......GLQNNLSPKTKGTPVHLGTI 410 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

length: 0 length: 200000000 sed 88 Minimum I Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq\_23Sep04:\*

1: geneseqp1980s:\*

2: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp201s:\*

6: geneseqp203s:\*

7: geneseqp203ss:\* geneseqp2004s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### STIMMARIES

	g	Human Tum	Human tum	Novel hum	Human mal	Novel hum	Novel hum	Human Tum	Human tum	Novel hum	Human ORF	Mouse Tum	Mouse Tum	Mouse tum	Mouse tum	Tumour en	Human tum	Human pro	uman pol	Stem cell	Human ste	Amino aci	Stem cell	Human PRO	Human pol	Kuman Tum
	Description	Abb90749 H	Abu54456 H	Adi21063 N	Adh13230 H	Adi21554 N	_	-	-	Adi21064 N	-	_			Abu54490 M	Aab85400 T			Aam39067 H	Aab85396 S	0	Aab31211 A	Aab85394 S	Aau29259 H	Aam39068 H	Abb90734 H
SUMMAKIES	ΩI	ABB90749	ABU54456	ADI21063	ADH13230	ADI21554	ADI21553	ABB90723	ABU54430	ADI21064	AAB43131	ABB90783	ABB90729	ABU54436	ABU54490	AAB85400	AB001434	ADB65558	AAM39067	AAB85396	AB001430	AAB31211	AAB85394	AAU29259	AAM39068	ABB90734
	DB	, s	9	7	œ	7	7	Ŋ	9	7	ო	S	'n	9	9	4	9	7	4	4	9	4	4	4	4	'n
	Length	200	200	200	200	527	527	1002	1002	488	400	200	200	200	200	431	431	240	486	499	499	529	529	529	529	529
de	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	96.2	86.7	81.1	81.1	81.1	81.1	80.9	80.9	54.8	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1
	Score	2218	2218	2218	2218	2218	2218	2218	2218	2134	1924	1799.5	1799.5	1799.5	1799.5	1795	1795	1215	1066.5	1066.5	1066.5	1066.5	1066.5	1066.5	1066.5	1066.5
	Result No.	1	2	٣	4	Ŋ	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB907569. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic

An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.

Claim 1; Page 206-207; 331pp; English.

Abb90726 Human Tum Abp53349 Human tra	Human Human	Abus8635 Human PRO Abu88183 Novel hum	Human	Human	Human	Abu82941 Human PRO	Novel	Abr68311 Human sec	Abu96364 Novel hum	Abu92795 Human sec	Abo08872 Human sec	Abo02924 Human sec	Abr75078 Human sec	Abr94840 Human sec	Abo25182 Novel hum
ABB90726 . ABP53349	ABG69157 ABG69161	ABU58635 ABU88183			-	ABU82941	ABU90062	ABR68311	ABU96364	ABU92795	ABO08872	ABO02924	ABR75078	ABR94840	AB025182
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1066.5	1066.5	1066.5	1066.5	1066.5	1066.5	1066.5	1066.5	1066.5	1066.5	1066.5	1066.5	1066.5	1066.5	1066.5	1066.5
26 27	7 7 8 7 8 7 8	30	35		35	9	7	8	39	40	41	42	43	44	45

# ALIGNMENTS

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Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                          Human Tumour Endothelial Marker polypeptide SEQ ID NO 230.
                                                                                                                                                                                                                                                                                   St Croix B, Kinzler KW, Vogelstein B;
ABB90749 standard; protein; 500 AA.
                                                                                                                                                                                                                     02-AUG-2000; 2000US-0225599P.
11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
                                                                                                                                                                                                    01-AUG-2001; 2001WO-US024031.
                                                                                                                                                                                                                                                               (UYJO ) UNIV JOHNS HOPKINS.
                                      (first entry)
                                                                                                                                                                                                                                                                                                     WPI; 2002-291856/33.
N-PSDB; ABL92103.
                                                                                                                                                             WO200210217-A2.
                                      30-MAY-2002
                                                                                                                                          Homo sapiens
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                                                                                                                         psoriasis.
                   ABB90749;
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                                                                                                                                                                                                                                                                  PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 137
                                                                                                                                                                                                                                                                                                           SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
                                                                                                                                                                                                                                                                                                                                  SPDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 197
                                                                                                                                                                                                                                                                                                                                                                                                                                           DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPFCLQHRSCDACMSSD 317
                                                                                                                                                                                                                                                                                                                                                                                     DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDISFSPYD 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleocide sequences: tumour endothelial markers (TEM) ABL921996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92041 and ABL92143-ABL92191; mormal
                                                                                                                                                                                                                     77
                                                                                                                                                                                            1 ALSPOPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL
                                                                                                                                                                                                            ALS POPGAGHDEGPGSGWAAKGTVRGWNRRARES PGHVSEPDRTQLSQDLGGGTLAMDTL
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                                                                                                                                                               Gaps
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                                                                                                                                 Length 500;
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                                                                                                                                                               Indels
                                                                                                                                  100.0%; Score 2218; DB 5; 100.0%; Pred. No. 2.7e-211;
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                                                                                                                                                               Mismatches
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06-FEB-2002;
                                                                                                       Sequence 500
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Kinzler KW, Vogelstein

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                           The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal polymucleoties equences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour andiogenesis, for for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumor endothelial
                                                      New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
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                                                                                                                                                                                                                                                                                                                                                                                                 Score 2218; DB 6;
; Pred. No. 2.7e-211;
0; Mismatches 0;
                                                                                                                                     Disclosure; Page 221-222; 374pp; English.
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           WPI; 2003-093016/08
N-PSDB; ABX72028.
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                                                                                                      psoriasis
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Predicting, diagnosing or prognosing malignant neoplasia by detecting at least two markers, where the markers are genes from one or more chromosomal regions altered in malignant neoplasia,.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          preventing or treating malignant neoplasia. The disease treated is preferably breast cancer. The present sequence is that of a human malignant neoplasia-related protein which may be used in the method of
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                                                                                                      GDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLONNLSPKTKGTPVHLGTI
                                                                          GDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTI
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1larity 100.0%; Pred. No. 2.7e-211;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                        Human malignant neoplasia-related protein SeqID79.
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                                                                                                                                                                                                                                               ADH13230 standard; protein; 500
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13-FEB-2003; 2003EP-00003112
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Best Local Similarity
Matches 410; Conserv
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ADH13230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptide are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the useful for raising antibodies, is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incitsions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
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       tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                  Wang J;
Wang D;
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Drmanac RT,
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Wehrman T, Weng G, Zhou P,
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                                                                                                                                                                                                19-SEP-2002; 2002WO-US029964.
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13-SEP-2002; 2002US-00323739.
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Best Local Similarity 100.
Matches 410; Conservative
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N-PSDB; ADI21779.
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Ghosh M, Xue AJ,
Haley-Vicente D;
                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 500 AA;
                                                                                                 WO2003025148-A2
                                                      Homo sapiens
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                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                 Sequence 527 AA;
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                                                                                                                                                                                            polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; lymphoid cell disorder; lymphoid cell disorder; lissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue replacement; burn; incision; ulcer; cancer; human.
                    PDNRTRVVEDNHSYYVGRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 137
                                                                           SPDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
                                                                                                       SPDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 197
                                                                                                                                                                          DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 300
                                                                                                                                                                                                                                                         DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPFCLQHRSCDACMSSD 317
                                                                                                                                                                                                                                                                                                              LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDTSFSPYD 360
                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang J;
Vang D;
PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL
                                                                                                                                                      GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS
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                                                                                                                                                                                                                                                                                                                                                                                           GDLTTISSSLFIDSLTIEDDIKLNPYAGGDGLQNNLSPKTKGTPVHLGTI 410
                                                                                                                                                                                                                                                                                                                                                                                                                GDLTTSSSLFIDSLTTEDDTKLNPYAGGDGLONNLSPKTKGTPVHLGTI 427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ren F, Zhang J, Zhao QA
ng G, Zhou P, Drmanac RT,
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Weng (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADI21554 standard; protein; 527
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-SEP-2001; 2001US-0323739P.
13-SEP-2002; 2002US-00323739.
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Ghosh M, Xue AJ, <sup>V</sup>
Haley-Vicente D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2003-354603/33.
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N-PSDB; ADI21334.
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The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
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; Pred. No. 3e-211;
0; Mismatches 0;
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(first entry)

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Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; attianglogenic; tumour; necembles; vescularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                               An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                          Human Tumour Endothelial Marker polypeptide SEQ ID NO 179.
                                                                                                                                                                                                                                                                                                                                                                                       St Croix B, Kinzler KW, Vogelstein
                                                                                                                                                                                                                                                                                                           11-AUG-2000; 2000US-0224360P.
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                                                                                                                                                                                                         WO200210217-A2.
                                                                                                                                                                              Homo sapiens,
                             30-MAY-2002
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                                                                                                                                               psoriasis.
 ABB90723;
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                                                                                                                                New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and replacement.
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                                            Wang J;
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                                                         Wang D;
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                                           Zhang J, Zhao QA,
ou P, Drmanac RT,
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                                           Goodrich RW, Ren F, Zhang
thrman T, Weng G, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 2218; DB 7
Pred. No. 3e-211;
Mismatches 0
                                                                                                                                                                                                                   Example 3; SEQ ID NO 804; 156pp; English.
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                                                       Wehrman T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 410; Conservative
                                                                                                  WPI; 2003-354603/33.
N-PSDB; ADI21333.
                                           Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                        Tang YT, Asundi V
Ghosh M, Xue AJ,
Haley-Vicente D;
               HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 527 AA;
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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a ABB90149, addothelial marker (TEM) protein selected from ABB90735, ABB90740, ABB90756 and ABB90765. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and are disclosed, as are marker oligonuclectide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (TEM) ABL91995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 2218; DB 5; Length 1002; 100.0%; Pred. No. 8e-211; ive 0; Mismatches 0; Indels 0;
Disclosure; Page 125-128; 331pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 410; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1002 AA;
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ABB90723 standard; protein; 1002 AA.

RESULT 7 ABB90723 ID ABB9

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forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; bone cartilage tissue growth; tendon tissue growth; ligament tissue growth; nerde tissue growth; regeneration; wound healing; tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
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                                                                                                                                                                                                                                                                                                                                                           DAFMILNPSPDVPESRRRSIFEYHRIBLDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 300
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                                                                                                               SPDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
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u P, Drmanac RT,
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13-SEP-2002; 2002US-00323739.
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Haley-Vicente D;
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                                                                                                        LIFINCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDTSFSPYD 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting necangiogenesis or tumour angiogenesis, for inducing an immune response to tumour andichelial cells in a patient, or for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention
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Gaps
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                                                                                                                                                               410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 122-124; 374pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     endothelial marker TEM 8.
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2002US-0354262P.
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N-PSDB; ABX72003.
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06-FEB-2002;
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The invention relates to an isolated polynucleotide encoding

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polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and otterates, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in regeneration, in wound healing, in tissue erpair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDTSFSPYD 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels 12;
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Pred. No. 6e-203;
0; Mismatches 0; Indels 1
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97.1%;
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nes 398; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 488 AA;
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Best Local 5
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AAC74446 to AAC77606 encode the proteins given in AB40237 to AAB43397,
which represent the human ORFX open reading frames 1 to 3161. The ORFX
cantipsoriatic; antiparkinsonian; octropic; hepatotropic; valnerary;
antipsoriatic; antiparkinsonian; wootropic; neuroprotective; osteopathic;
anticonvalsant; antiarthritic; immunosuppresent; immunostimulant;
cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
dermatological; immunosuppressive; antidiabetic; hypotensive;
dermatological; antirheumatic; antidiabetic; hypotensive;
cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
dermatological; antirheumatic; antithyroid; and antianaemic. The
sequences can be used for determining the presence of or predisposition
cc, or preventing or treating pathological conditions associated with an
CORFX-associated disorder. The nucleic acids can be used to express ORFX
proteins in gene therapy vectors. The proteins and nucleic acids may be
used to treat cancers, proliferative disorders, neurodegenerative
disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
disorders mellitus, hypertension, hypothyroidism, cholesterol ester
storage, systemic lupus erythematosus, severe combined immunodeficiency
(SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
enhance coagulation; to inhibit thrombosis; and as a contraceptive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL
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bone damage; cartilage damage; antiinflammatory disease; coagulation;
thrombosis; contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
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                                                                                                                                                                                                                                      31-MAR-1999; 99US-0127607P.

02-APR-1999; 99US-0127636P.

05-APR-1999; 99US-0127728P.

30-MAR-2000; 2000US-00540763.
                                                                                                                                                                                             31-MAR-2000; 2000WO-US008621
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                                                                                                                                                                                                                                                                                                                                                                                             Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-602362/57.
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                                                                                                            WO200058473-A2.
                                                                   Homo sapiens.
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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neconglogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM
                                                                                                                                                                                                                                                                                     SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
                                                                                                  139 SFDFPFYGHPLRQITIATGGFIFMGDMLHRMLTATQYVAPLMANFNPGYSDNSTVAYFDN 198
                                                                                                                                                                                                   DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 300
                                                                                                                                                                                                                                                                   301 LTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDTSFSPYD 360
   PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; pan-endothelial marker; immunostimulant; antianglogenic; tumour; necangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; psoriasis.
                                                                                                                                     GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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                                                                                                                                                                                                                                                                                                                                                       Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 192.
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11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
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                                                                                                                                                                                                                                                                                                        cytostatic;
                                                                                                                                                                                                                                                                                     Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic normal endothelial marker; pan-endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis; psoriasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALSPATPAGHNEGODSAWTAKRTROGWSRRPRESPAQVLKPGKTQLSODLGGGSLAIDTL
1 ALSPOPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
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                                                     LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDT 354
                                                                        LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRWCEDFQDEDHDSASPDT
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                                                                                                                                                                                                                                                                     Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 297.
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                                                                                                                                                                    ABB90783 standard; protein; 500 AA
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11-AUG-2000; 2000US-0224360P.
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Matches 331; Conservative
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N-PSDB; ABL92136.
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  are disclosed, as are marker oligonucleotide sequences: tumour: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers (PEM) ABL91903-ABL91995
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genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789)
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                                                                                                                       1 ALSPOPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL
                                                                                                                                                PONRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL
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                                                                        81.1%; Score 1799.5; DB 5
80.7%; Pred. No. 1.2e-169;
                                                                                          39; Mismatches
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2002US-0354262P.
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Best Local Similarity
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                                                      Sequence 500 AA;
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06-FEB-2002;
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                                                                                                                                                               The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal endothelial marker (TEM), normal endothelial marker (PEM), and pan-endothelial marker (PEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour endothelial cells in a patient, or sequence represents a mouse TEM protein
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       marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis psoriasis.
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  designated
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  protein,
                                                                                                                     Disclosure; Page 147-148; 374pp; English
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                                                                                                                                                                                                                                                                                          New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.
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ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
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                                                                                                                                                                                                                            Kinzler KW,
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 339-340; 374pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence represents a mouse TEM protein
                                                                                                                                                                                                                            St Croix B,
                                                                                                                    10-APR-2002; 2002WO-US008253
                                                                                                                                                 11-APR-2001; 2001US-0282850P.
06-FEB-2002; 2002US-0354262P.
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N-PSDB; ABX72061.
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The invention provides novel human stem cell growth factor-like polypeptides and polymelotides encoding them. The polypeptides having stem cell growth factor-like activity, can be expressed by standard recombinant methodology. The polymolocides and polypeptides can be used to induce differentiation of embryonic and adult stem cells to give rise to different cell types. They may also be used in the treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease. They may also be utilized to generate new tissues and organs that may aid supplements. The present sequence represents a tumour endothelial marker applements. The present sequence represents a tumour endothelial marker applements protein, homologous to a stem cell growth factor-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stem cell growth factor-like polypeptide; leukemia; hemophilia; human; degenerative disease; hutritional supplement; cytostatic; nootropic; neuroprotective; hemostatic; antisense-therapy; gene-therapy; tumour endothelial marker 7 precursor protein.
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                                                                                                                                                                                               endothelial marker 7 precursor protein.
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   standard; protein; 431
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21-JAN-2000; 2000US-00488725.
7-APR-2000; 2000US-00545714.
11-APR-2000; 2000US-00547358.
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                                                                                                                                 17-SEP-2001
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SOMMERCES	ΩΙ	US-09-918-715-230	US-10-435-696-79	US-10-474-794-230	US-10-357-819-2	US-09-918-715-179	US-10-474-794-179	US-10-357-819-4	US-10-156-487A-5	US-09-918-715-192	US-09-918-715-297	US-10-156-487A-6	US-10-474-794-192	US-10-474-794-297
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Sequence 36, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 31, Appl Sequence 131, Appl Sequence 189, Appl Sequence 47, Appl Sequence 472, Appl	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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## ALIGNMENTS

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GOUTH STATES APPLICATION US/09918715  UNDICATION NO. US20030017157A1  BENERAL INFORMATION: APPLICANT: BEAT VOGEISTEIN APPLICANT: BEAT VOGEISTEIN APPLICANT: BEAT VOGEISTEIN TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS FILE REFERENCE: 1107.00134 FILE REPERENCE: 107.00134 FRICK RAPLICATION NUMBER: 60/222, 599 FRICK APPLICATION NUMBER: 60/222, 599 FRICK RAPLICATION NUMBER: 60/224, 360 FRICK RELING DATE: 2000-08-12 FRICK RELING DATE: 2000-08-11 FRICK DATE: 20	Score 2218; DB 10; Length 500; Pred. No. 1.5e-203; 0; Mismatches 0; Indels 0; Gaps 0;	ALSPOPGAGHDEGPCSGWAAKGTVRGWNRRARESPGHVSEPDRTOLSODLGGGTLAMDTL 60	PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120
1-715-230 12 230, Application US/09918715 12 100 No. US20030017157A1 12 INFORMATION: 13 ANT: Bard St. Croix 14 ANT: Bart Vogelstein 14 ANT: Bert Vogelstein 15 ANT: Kenneth Kinzler 16 TOF INVENTION: ENDOTHELIAL CELL 17 FILING DATE: 2001-08-01 17 FILING DATE: 2000-08-02 18 APPLICATION NUMBER: 60/224,360 18 TLING DATE: 2000-08-01 18 APPLICATION NUMBER: 60/224,360 19 APPLICATION NUMBER: 60/224,360 11 APPLICATION NUMBER: 60/224,360 11 APPLICATION NUMBER: 60/228,850 11 APPLICATION NUMBER: 60/282,850 11 APPLICATION NUMBER: 60/2820 1	100.0%; 100.0%; vative	GAGHDEGPGSGWA             GAGHDEGPGSGWA	VVEDNHSYYVSRL
Sequence 230, Application US/09918715 Sequence 230, Application US/09918715 Publication No. US20030017157A1 GENERAL INFORMATION: APPLICANT: Bert Vogelstein APPLICANT: Bert Vogelstein APPLICANT: Kenneth Kinzler TTTLE OF INVENTION: ENDOTHELIAL CELL EXPR. FILE REPERBNCE: 1107.00134 CURRENT APPLICATION NUMBER: 06/9918,715 CURRENT FILING DATE: 2001-08-01 FRIOR PRICH PRICH DATE: 2000-08-02 FRIOR PRILING DATE: 2000-08-11 FRIOR FILING DATE: 2000-08-11	atch sal Simi 410;	1 ALSPQP        18 ALSPQP	61 PDNRTR 
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318 LIFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDTSFSPYD 377
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APPLICANT: Carson-Walter, Bleanor
APPLICANT: Carson-Walter, Brad
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: 05/10/474,794
CURRENT PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
IENGTH: 500
                                                                                                                                                                                                                                           US-10-474-794-230
; sequence 230, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
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APPLICANT: Alvarez, Enrique; APPLICANT: Edinger, Shlomit R.
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Best Local Similarity 100.
Matches 410; Conservative
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US-10-357-819-2
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| Publication No. US20040018525A1
| Sequence 79, Application US20040018525A1
| GENERAL INFORMATION:
| APPLICANT: Wirtz, Ralph
| APPLICANT: Munnes, Marc
| APPLICANT: Munnes, Marc
| APPLICANT: Munnes, Marc
| TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
| TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
| FILE REFERENCE: LeA 36 108
| CURRENT APPLICATION NUMBER: EP03003112.4
| PRIOR PELING DATE: 2003-05-09
| PRIOR PELING DATE: 2003-05-13
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     PDNRTRVVEDNHSYYVSRLYGPSEPHSRELMVDVAEANRSQVKIHTILSNTHRQASRVVL 137
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US-10-435-696-79
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US-10-435-696-79
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                                                                                                                                                                                                                                                               Sequence 179, Application US/09918715
; Sequence 179, Application US/09918715
; Publication No. US20030017157A1
; GENERAL INFORMATION:
    APPLICANT: Bard St. Croix
; APPLICANT: Bert Vogelerein
; APPLICANT: Kenneth Kinzler
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REPERENCE: 1107.00134
; CURRENT FILING DATE: 2001-08-01
; PRIOR PILING DATE: 2000-08-02
; PRIOR PILING DATE: 2000-08-11
; PRIOR PILING DATE: 2000-08-11
; PRIOR PILING DATE: 2000-04-11
; PRIOR FILING DATE: 2000-04-11
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US-10-474-794-179
IS-10-474-794-179
; Sequence 179, Application US/10474794
; Publication No. US20040213793A1
; GENERAL INFORMATION:
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US-09-918-715-179
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APPLICANT: Miller, Charles E.
APPLICANT: Padigaru, Meera
APPLICANT: Patturain, Meera
APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Rieger, Daniel K.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shimkers, Richard A.
APPLICANT: Spyck, Kimberly A.
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      240
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                                                                                                                                                                                                                                                                                                                                                                                                                             THILE REPERINCE: 21402-538A

CURRENT APPLICATION NUMBER: US/10/357,819

CURRENT PILING DATE: 2003-02-03

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-05-31

PRIOR PLING DATE: 2000-05-31

PRIOR PELING DATE: 2001-02-14

PRIOR FILING DATE: 2001-02-14

PRIOR FILING DATE: 2002-02-25

PRIOR PELING DATE: 2002-02-25

PRIOR PELING DATE: 2002-02-19

PRIOR PELING DATE: 2002-02-20

PRIOR PELING DATE: 2002-02-21

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Gangolli, Esha A.
Gerlach, Valerie L
Gorman, Linda
Guo, Xiaojia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 410; Conservative
                                                                                               Ji, Weizhen
Kekuda, Ramesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-10-357-819-2
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APPLICANT: SINGRES, KINDERIA A.
APPLICANT: STORG, Mei
APPLICANT: STORG, Mei
APPLICANT: Zhong, Mei
APPLICANT: Zhong, Mei
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD:
FILE REPRERNCE: 21402-538A
CURRENT APPLICATION NUMBER: US/10/357,819
CURRENT FILING DATE: 2000-103-08
FRICR FILING DATE: 2000-103-08
FRICR FILING DATE: 2000-05-31
FRICR FILING DATE: 2000-05-31
FRICR FILING DATE: 2000-02-25
FRICR FILING DATE: 2002-02-25
FRICR FILING DATE: 2002-02-25
FRICR FILING DATE: 2002-02-01
FRICR FILING DATE: 2002-02-01
FRICR FILING DATE: 2002-02-01
FRICR FILING DATE: 2002-02-01
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Best Local Similarity 97.1%; Pred. No. 1.7e-195;
Matches 398; Conservative 0; Mismatches 0;
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18-10-156-487A-5
Sequence 5, Application US/10156487A
Publication No. US20030092025A1
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APPLICANT: St. Croix, Brad
APPLICANT: Vogelaterin, Bert
APPLICANT: Vogelaterin, Bert
APPLICANT: Kincler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPERBNEE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR APPLICATION NUMBER: 60/382,850
PRIOR APPLICATION NUMBER: 60/382,850
PRIOR PILING DATE: 2001-04-11
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1002
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100.0%; Pred. No. 4.5e-203;
tive 0; Mismatches 0;
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Publication No. US20040259774A1
GENERAL INFORMATION:
APPLICANT: Edinger, Shlomit R.
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gengal, Saha A.
APPLICANT: Gorman, Linda
APPLICANT: Kekuda, Ramesh
APPLICANT: Kekuda, Ramesh
APPLICANT: Miller, Charles E.
APPLICANT: Miller, Charles E.
APPLICANT: Patturajan, Meera
APPLICANT: Ratelli, Luca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 410; Conservative
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US-10-474-794-179
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US-10-357-819-4
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GENERAL INFORMATION:
APPLICANT: Juan, Todd
APPLICANT: Bass, Michael B.
APPLICANT: Bass, Michael B.
APPLICANT: Oliner. John
TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
FILE REFERENCE: 01-072-A
CURRENT APPLICATION NUMBER: US/10/156,487A
CURRENT FILING DATE: 2002-09-10
PRIOR APPLICATION NUMBER: 60/293,852
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 137
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| Publication No. US20030017157A1
| GENERAL INFORMATION:
| APPLICANT: Brad &t. Croix
| APPLICANT: Bert Vogelstein
| APPLICANT: Renneth Kinzler
| TITLE OF INVENTION: RNDOTHELIAL CELL EXPRESSION PATTERNS
| FILE REFERENCE: 1107.00134
| CURRENT PLILOSTION NUMBER: US/09/918,715
| CURRENT PLILOSTION NUMBER: 60/222,599
| PRIOR PPLICATION NUMBER: 60/224,360
| PRIOR PLILOSTION NUMBER: 60/282,850
| PRIOR PLING DATE: 2000-04-11
| NUMBER OF SEQ ID NOS: 358
| LENGTH: 500
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95.0%; Pred. No. 1.5e-191;
iive 0; Mismatches 7;
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Best Local Similarity 95.0
Matches 397; Conservative
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ORGANISM: Homo sapiens
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US-09-918-715-192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Bert CO. LOLL
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHBLIAL CELL EXPRESSION PATTERNS
TITLE OF ILLNG DATE: 2001-08-01
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR PILING DATE: 2000-08-01
PRIOR PILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
NUMBER OF SEQ ID NOS: 358
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                          Query Match 81.1%; Score 1799.5; DB 10; Lengt
Best Local Similarity 80.7%; Pred. No. 2.2e-163;
Matches 331; Conservative 39; Mismatches 39; Indels
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Publication No. US20030017157A1
GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-918-715-192
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Matches 331;
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241 DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 300
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               GD-STTSSSLFIDSLITEDDIKINPYAEGDGLPDHSSPKSKGPPVHLGTI
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                                                                                                     Sequence 192, Application US/10474794

publication No. US20040213793A1

GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: T. Vogelstein, Bert
APPLICANT: Nogelstein, Bert
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPRENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2001-014
PRIOR APPLICATION NUMBER: 60/382,850
PRIOR APPLICATION NUMBER: 60/308,829
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 359
SOFTWARE: FRAGERQ for Windows Version 4.0

SEQ ID NO 192
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Publication No. US20040213793A1

GENERAL INFORMATION:
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Wogelstein, Bert
APPLICANT: Wogelstein, Bert
APPLICANT: Wogelstein, Kenneth
APPLICANT: AFINIER. Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
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80.7%; Pred. No. 2.2e-163;
tive 39; Mismatches 39;
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Matches 331; Conservative
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                                                                                                 US-10-474-794-192
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US-10-474-794-297
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                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bass, Michael B.
APPLICANT: Dincr.
TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
FILE REFERENCE: 01-07-A
CURRENT APPLICATION NUMBER: US/10/156,487A
CURRENT PILING DATE: 2002-09-10
PRIOR PILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 500
                                  SEDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/10156487A; Publication No. US20030092025A1
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APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Chao, Cheng-Chi
APPLICANT: Dramane, Radoje T
APPLICANT: Lee, Juhi
APPLICANT: Lee, Juhi
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERENCE: 30266/37630
CURRENT APPLICATION NUMBER: US/10/168,365
CURRENT FILING DATE: 2000-12-22
CURRENT FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PATENTIN VERSION 3.0
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                           1 LAMDTLEDDNRTRVVEDNHSYYVSRLYGPSEPHSRELWYDVAEANRSQVKIHTILSNTHRQ
                                                                            115 ASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST
                                                                                                                                                      VVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKBIPMSVPEISSSQHP
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Pred. No. 4.8e-163;
0; Mismatches 7;
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Best Local Similarity 94.2
Matches 343; Conservative
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Publication No. US20030022825A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/374BER: US/09/912,935
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR PILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN VERSION 3.0
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Pred. No. 2.2e-163;
9: Mismatches 39; Indels
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94.2%; Pred. No. 4.8e-163;
iive 0; Mismatches 7;
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CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/208,829
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 297
LENGTH: 500
                                                                                                                                                                                                                                                                                     81.1%;
80.7%;
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 80.7<sup>3</sup>
Matches 331; Conservative
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 343; Conserv
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; ORGANISM: Mouse
US-10-474-794-297
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Search completed: January 28, 2005, 22:19:20 Job time : 113.059 secs

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January 28, 2005, 21:55:58 ; Search time 7.47922 Seconds (without alignments) 1389.370 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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1 LSFDFPFYGHPLRQITIATG......LHHDGRIVFAYKEIPMSVPE 108 US-09-918-715-230\_COPY\_137\_244 588 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB E Maximum DB E

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	nidogen precursor	alpha tectorin - c	sodium channel pro	L-fucose-specific	alpha tectorin - m	extracellular nucl	hypothetical prote	3-oxoacyl-[acyl-ca	3-oxoacyl-(acyl-ca	vitamin B12 recept	class I histocompa	phosphoenolpyruvat	heme d1 synthesis	transporter, NadC	transport system p	vitamin b12 recept			hypothetical prote	procollagen-lysine	vitamin B12 recept	procollagen-lysine	hypothetical prote	class I histocompa	outer capsid prote	outer capsid prote	probable oxidoredu	probable membrane
SUMMARIES	, QI	T19786	S31213	T30243	A60165	JC7853	T30197	874915	E71086	A97919	C95048	S77723	JH0289	S18606	JC4553	B82510	B64232	QRECBT	A98241	F86088	H71981	T08679	AB0935	S59964	T16305	JH0288	VPXRMN	VPXR16	A85758	B64877
	DB	~	-		7		7	7	7	7	~	7	~	7	7	7	~	-	7	~				~		7	-	-	7	,7
	Length	476	1161	2120	1321	310	2155	1879	4436	324	324	337	356	535	392	462	543	614	614	614	330	365	614	728	2214	362	280	280	401	401
de	Query Match	.54.0	20.9	14.3	14.2	13.4	13.3	12.4	12.4	11.6	11.6	11.6	11.5	11.5	11.4	11.4	11.4	11.4	11.4	11.4	11.2	11.2	11.2	11.2	11.1	11.1	10.9	•	10.9	10.9
	Score	317.5	123	84	83.5	79	78		73	68	68	68	67.5	67.5	67	67	67	67	67	67	99	99	99	99	65.5	65	64	64	64	64
	Result No.	П	~	m	4	Ŋ	9	7	8	6	10	11	12	13	14	15	16	17	18	19			22	23		25		27	28	29

RESULT 2

Journal precursor - sea squirt (Halocynthia roretzi)
NyAlternate names: entactin
Cispecies: Halocynthia roretzi
Cispecies: Jo-Sep-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004
CiAccession: S31213
Bur. J. Biochem. 213, 11-19, 1993
Bur. J. Biochem. 213, 11-19, 1993
A;Title: Ascidian entactin/nidogen. Implication of evolution by shuffling two kinds of c
A;Reference number: S31213, MUID:93238676; PMID:8477687
A;Reference number: S31213
A;Accession: S31213
A;Accession: S31213
CiSpecies: 1-1161 <NAKA
A;Residues: 1-1161 <NAKA
A;Residues: 1-1161 <NAKA
Cross-references: UNIPROT:Q04901; EMBL:D14038; NID:g217363; PIDN:BAA03127.1; PID:g2173
C;Superfamily: Ascidian nidogen; EGF homology; LDL receptor YWTD-containing repeat homol
C;Keywords: basement membrane; collagen binding; disulfide bond; duplication; extracellu
F;1-20/Domain: signal sequence #status predicted <SIG>

probable oxidoredu pregnancy-specific	pregnancy-specific	reaction center co	outer layer protei	probable polyketid	cytochrome c oxida	conserved hypothet	lysine specific pe	glutamine-fructose	hypothetical prote	conserved hypothet	conserved hypothet	60S ribosomal prot	pregnancy-specific
D90861 B36109	A34595	T31454	VPXRW9	T28702	G97742	G89877	A86899	B72412	D71073	A95064	C97931	D90134	D33258
01 01	<b>~</b> ~	9 7	-	~	N	N	N	~	0	~	7	7	0
401	424	609	176	1407	337	390	206	909	189	243	264	375	435
10.9	10.9	10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.7	10.7	10.7	10.7	10.7
64 64	4 4	64	64	64	63.5	63.5	63.5	63.5	63	63	63	63	63

# ALIGNMENTS

T19786 T19786 T19786 C;Species: Caenor C;Date: 15-Oct-19 C;Accession: T197 R;Milkinson, J; Submitted to the A;Reference numbe A;Reference numbe A;Reference type: A;Retus: prelimi A;Molecule type: A;Residues: 1476 A;Cross-reference A;Reperimental so C;Genetics: C;Genetics: C;Genetics: A;Map position: 3 A;Introns: 23/1; C;Superfamily: Ca	RESULT 1 T19786 T19786 T19786 C; Pate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Accession: T19786 R; Wilkinson, J; Barlow, K. Submitted to the EMBL Data Library, August 1994 A; Reference number: Z19177 A; Accession: T19786 A; Residues: 1-476 < WIL. A; Map position: 3 A; Map position: 3 A; Map position: 3 A; Introms: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2 C; Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3
Query Ma Best Loc Matches	Ouery Match 54.0%; Score 317.5; DB 2; Length 476; Best Local Similarity 55.7%; Pred. No. 4.5e-26; Matches 59; Conservative 19; Mismatches 27; Indels 1; Gaps 1;
o o o	1 LSFDFPFYGHPLRQITIATGGF1FMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 60
à da	61 NGTVFVVQMDHVYLQGWEDKGSFTFQAALHHDGRIVFAVKEIPMSV 106 

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A;Title: Nucleotide sequence of the putative sodium channel gene from Drosophila: the for A;Reference number: S04029; MUID:88040482; PMID:2444928
A;Accession: S04029
                                                                                                                                  A, Residues: 1-362,363-626,627-1321 <SAL>
A, Cross-references: UNIPROT: Q27930; EMBL:X14394
B, Salkoff, L.; Butler, A.; Wei, A.; Scavarda, N.; Giffen, K.; Ifune, C.; Goodman, R.; Ma: Science 237, 744-749, 1987
A, Title: Genomic organization and deduced amino acid sequence of a putative sodium chann A, Reference number: A60165; MUID:87292090; PMID:2441469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Molecule type: protein
A,Residues: 132-147,148-177 <1S2>
C,Comment: This protein, with ferrichrysin-affinity, has hemagglutination activity again
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding a fucose-specific le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: FlyBase:NaCP60E
A;Cross-references: FlyBase:FBgn0002920
A;Introns: 237/2; 310/3; 362/3; 414/3; 471/3; 531/3; 581/1; 626/3; 751/2; 801/1; 908/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Aspergillus oryzae
C;Date: 18-Nov-2002 #sequence_revision 18-Nov-2002 #text_change 09-Jul-2004
C;Date: 18-Nov-2002 #sequence_revision 18-Nov-2002 #text_change 09-Jul-2004
C;Accession: 407853, PC719, Hata, Y.; Kawato, A.; Suginami, K.; Abe, Y.; Imayasu, Biosci. Biotechnol. Biochem. 66, 1002-1008, 2002
A;Title: Molecular cloning and overexpression of fleA gene encoding a fucose-speci A;Reference number: 407853; MUID:22087106; PMID:12092808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 GHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDNGTVFVVQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alpha tectorin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T30197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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llarity 45.2%; Pred. No. 0.78;
Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                A)Residues: 40-355;363-560,'P',562-626;632-1263 <8A2>
A)Cross-references: RWBL:X14394
A;Note: part of this sequence was confirmed by mRNA sequencing
A;Note: the authors' translation is shown at position 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 NFNPGYSDNSTVVYFDN--GTVFVVQWDHVYLQGWEDKGSFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Molecule type: DNA
A,Residues: 1-310 <ISH>
A,Cross.references: UNIPROT:QBTGE0; DDBJ:AB072379
A,Experimental source: strain OSI1018
A,Accession: PC7191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
14.2%; Score 83.5; DE
Best Local Similarity 31.1%; Pred. No. 1.5;
Matches 19; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 0.78
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L-fucose-specific lectin - Aspergillus oryzae
                                                                                                                                                                                                                                                                                                                                                   A;Status: nucleic acid sequence not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Introns: 12/1; 71/3; 143/1; 177/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 19; Conserv
                                                                                                           A, Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                            A; Accession: A60165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 M 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
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Matches
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Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Gallus gallus (chicken)
Cispecies: Objectorian: Gallus gallus (chicken)
Cispecies: Objectorian: T30243
Ricoutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P.
Ricoutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P.
A.Title: Chick alpha tectorin: molecular cloning and expression during embryogenesis.
A.Reference number: Z20783; MUID:99251817; PMID:10320099
A.Accession: T30243
A.Accession: T30243
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-2120 <COU>
A.Residues: 1-2120 <COU>
A.Residues: 1-2120 <COU>
A.COUS
A.COUSE-reference: UNIPROT:09YH85; EMBL:AJ012287; NID:e1361091; PID:e1361092; PIDN:CAAC
A.Note: non-collagenous protein only expressed in the inner ear
F;21-1161/Product: nidogen #status predicted <MAT>
F;274-306/Domain: EGF homology <EG1>
F;574-316/Domain: BGF homology <EG1>
F;560-574/Region: 3-residue repeats (R-P-V)
F;603-673/Domain: thyroglobulin type I repeat homology <THY1>
F;686-748/Domain: thyroglobulin type I repeat homology <THY2>
F;686-748/Domain: thyroglobulin type I repeat homology <THY2>
F;900-943/Domain: LDL receptor YMTD-containing repeat homology <YM1>
F;944-986/Domain: LDL receptor YMTD-containing repeat homology <YM2>
F;987-1031/Domain: LDL receptor YMTD-containing repeat homology <YM3>
F;032-1075/Domain: LDL receptor YMTD-containing repeat homology <YM4>
F;1075-1114/Domain: LDL receptor YMTD-containing repeat homology <YM5>
F;1076-1114/Domain: EGF homology <EG2>
F;1077-1188/Domain: EGF homology <EG2>
F;107,334,360,484/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --FNPGYSDNSTVVY-------PDNGTVFVVQWDHVYLQGWEDKGSFTFQAA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A60165
sodium channel protein - fruit fly (Drosophila melanogaster) (fragments)
sodium channel protein - fruit fly (Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Species: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
C;Accession: S04029; A60165
S;Salkoff, L.; Butler, A.; Scavarda, N.; Wei, A.
Nucleic Acids Res. 15, 8569-8572, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LSFDFPFYGHPLRQITIATGGFIFMGDVIHR------MLTATQYVAPL-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 LSFDFPFYGHPLRQITIATGGFIFM-----GDVIHRMLTATQYVAPLMAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.3%; Score 84; DB 2; Length 2120; Best Local Similarity 27.1%; Pred. No. 2.3; Matches 38; Conservative 14; Mismatches 46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
20.9%; Score 123; DB 1; Length 116
Best Local Similarity 28.0%; Pred. No. 7.7e-05;
Matches 40; Conservative 18; Mismatches 41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : || || || || 158 SATEAIFLYPQDGLAVGE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LHHDGRIVFA---YKEIPMSVPE 108
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QAVLITDGVSSFAIFNYQEI 186
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12:53:51

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Wed Feb

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M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi DNA Res. 5. 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a A;Reference number: A71000; MUID:98344137; PMID:9679194
                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-4436 <KAW>
A;Residues: 1-4436 <KAW>
A;Cross-references: UNIPROT:058659; GB:AP000004; NID:g3236131; PIDN:BAA30051.1; PID:d103
A;Experimental source: strain OT3
A;Experimental sources strain OT3
A;Note: A;Note: a sequence replaced by GenBank
C;Genetics:
                                                                                                                                                                                                         A;Accession: E71086
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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hypothetical protein PH0954 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C;Date: 11-7086
C;Accession: E71086
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
R; Legan, P.K.; Rau, A.; Keène, J.N.; Richardson, G.P.
J. Biol. Chem. 272, 8791-8801, 1997
A; Title: The mouse tectorins. Modular matrix proteins of the inner ear homologous to com A; Reference number: 220771; MUID:9728643; PMID:9079715
A; Accession: T30197
A; Accession: T30197
A; Accession: T30197
A; Accession: T30197
A; Carose-references: UNIPROT:008523; EMBL; X99805; NID:g1915908; PIDN:CAA68138.1; PID:g191
A; Crosse-references: UNIPROT:008523; EMBL:X99805; NID:g1915908; PIDN:CAA68138.1; PID:g191
A; Experimental source: strain CD1; Whole cochleae
A; Note: non-collagenous protein only expressed in the inner ear, by cells both in and su
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              extracellular nuclease - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein sl10656
N;Alternate names: protein sl10656
S;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S74915
R;Kaneko, T; Sato, S; Kotani, H; Tanaka, A; Asamizu, E; Nakamura, Y; Miyajima, N; O, K.; Okumura, S; Shimpo, S; Takeuchi, C; Wada, T; Watanabe, A; Yamada, M; Yasuda
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A; Residues: 1-1879 < KANN
A; Cross-references: UNIPROT: P72938; EMBL: D90902; GB: AB001339; NID: g1652027; PIDN: BAA1695
A; Obsert he nucleotide sequence was submitted to the EMBL Data Library, June 1996
A; Genetics:
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A;Status: nucleic acid sequence not shown; translation not shown
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Best Local Similarity 26.3$
Matches 31; Conservative
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A;Molecule type: DNA
A;Residues: 1-324 «KUR»
A;Cross-references: UNIPROT:093NA1; GB:AE007317; PIDN:AAK99181.1; PID:g15457938; GSPDB:G
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R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, B.S.; P. R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; J. Bacteriol. 183, 5709-5717, 2001
A; Athuhors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R., A; Reference number: A97872; MUID:21422245; PMID:11544234
                                                                                                                                                                        162 SDVIFGLDEDLVTYDGYLLLVNLQDKIVIEWLASTYEDYESEIVDNINFQVIINSNGTIT 221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Streptococcus pneumoniae
Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
                                                                                                                                          1 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD
                                                                                                                                                                                                                                          --GSFTFQAALHHDGRIV
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                                                                                          36;
                                          Length 4436;
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                                                                                          Indels
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C;Superfamily: 3-oxoacyl-[acyl-carrier-protein] synthase III
C;Keywords: acyltransferase
                                                                                          43;
                                          12.4%; Score 73; DB 2;
17.8%; Pred. No. 84;
tive 27; Mismatches 43
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FAIRDVAKSIKQ 231
                                                                                                                                                                                                                                                                                                                                       FAYKEIPMS 105
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                                                                 Best Local Similarity
Matches 23; Conserv
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A; Gene: PH0954
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11.5%;
21.3%;
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Best Local Simi
Matches 30;
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S77723
vitamin B12 receptor - Citrobacter freundii (fragment)
C;Species: Citrobacter freundii
C;Species: Citrobacter freundii
C;Species: Citrobacter freundii
C;Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
C;Accession: S77723
R;Ward, R.J.; Glass, R.E.
Mol. Microbiol. 16, 813-815, 1995
A;Title: The 3'-terminal half of the btuB gene of Citrobacter freundii defines essential
A;Reference number: S77723
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-377 <WAR>
A;Residues: 1-377 <WAR>
A;Genetics:
C;Genetics:
A;Genetics:
A;Genetics: membrane protein; vitamin B12 transport
C;Supperfamily: vitamin B12 receptor; tonB-dependent receptor amino-terminal homology; tc
C;Keywords: membrane protein; vitamin B12 transport
F;85-337/Domain: tonB-dependent receptor carboxyl-terminal homology <TNC>
3-oxoacyl-(acyl-carrier-protein) synthase III [imported] - Streptococcus pneumoniae (stq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 GTVFVV----QWDHVYLQGWEDKGS------FTFQAA----LHHDGRIV-- 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 11.6%; Score 68; DB Similarity 23.5%; Pred. No. 12; 31; Conservative 19; Mismatches
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FAIRDVAKSIKQ 231
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RESULT 12

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C;Accession: JH0289
R;Yuhki, N.; O'Brien, S.J.
Bxp. Med. 172, 621-630, 1990
A;Title: DNA recombination and natural selection pressure sustain genetic sequence diver A;Reference number: JH0288; MUID:90324882; PMID:1695669
A;Accession: JH0289
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Rydcession: S18606
Rydcession: S18606
Rydcession: S18606
Rydride: 230, 257-269, 1991
AyTitle: Site-directed mutagenesis and DNA sequence of pckA of Rhizobium NGR234, encoding AyReference number: S18606; MUID:92079905; PMID:1720862
AyAccession: S18606
                                                                                                                                                                                                                                                                                                                                                                                      A,Cross-references: UNIPROT:Q95485; GB:U07672; NID:g467252; PIDN:AAA19462.1; PID:g467253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CKEywords: transmembrane protein
Fil-18/Domain: signal sequence (fragment) #status predicted <SIG>Fil-18/Domain: signal sequence (fragment) #status predicted <MAT>Fil9-356/Product: class I histocompatibility antigen #status predicted <MAT>Fil9-108/Domain: alpha-1 <ALI>Fil9-200/Domain: alpha-2 <ALI>Fil9-200/Domain: alpha-3 <ALI>Fil9-214-279/Domain: immunoglobulin homology <IPMN>Fil9-33-323/Domain: transmembrane #status predicted <TDO>Fil9-33-323/Domain: intracellular #status predicted <INT>
antigen precursor (clone FLA-B9) - cat (fragment)
                                    C;Species: Felis silvestris catús (domestic cat)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 27-Oct-2003
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C;Superfamily: phosphoenolpyruvate carboxykinase [ATP]
C;Keywords: carbon-carbon lyase; carboxy-lyase; nucleotide binding; P-loop
F;234-241/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: spleen
C; Superfamily: class I histocompatibility antigen; immunoglobulin homology
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24.8%; Pred. No. 16;
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Pred. No. 25;
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23 IFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGS 82

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Search completed: January 28, 2005, 22:12:39 Job time : 9.47923 secs
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104 FALAAAMHHQG 114
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A; Residues: 1-392 «KMA»
A; Residues: 1-392 «KMA»
A; Cross-references: UNIPROT: Q51480; DDBJ: D50473; NID: g1217594; PIDN: BAA09066.1; PID: g121
A; Experimental source: RM31
R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bx adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Nature 406, 959-964, 2000
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R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Acadardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82510
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-462 < HEI>
A;Experimental source: serogroup O1; strain N16961; biotype E1 Tor
                                                                                C;Species: Pseudomonas aeruginosa
C;Date: 12-Mar-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C;Accession: JG4553; H83581
R;Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A;Title: Sequencing and characterization of the downstream region of the genes encoding y for biosynthesis of heme dl.
A;Reference number: JC4552; MUID:96144254; PMID:8566817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathd A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83581
A;Status: preliminary
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A,Residues: 1-392 <STO>
A,Cross-references: GB.AE004488, GB.AE004091, NID:g9946372, PIDN:AAG03905.1, GSPDB.GN001
A,Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transporter, NadC family VCA0025 [imported] - Vibrio cholerae (strain N16961 serogroup C;Species: Vibrio cholerae C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 C;Accession: B82510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
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Best Local Similarity 28.2%; Pred. No. 20;
Matches 22; Conservative 10; Mismatches 30; Indels 16; Gaps
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11.4%; Score 67; DB 2; Length 462;
Best Local Similarity 23.9%; Pred. No. 24;
Matches 17; Conservative 14; Mismatches 26; Indels 14;
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A,Gene: nirF, PA0516
C,Superfamily: Pseudomonas stutzeri heme dl synthesis protein nirF
                                                      heme dl synthesis protein nirF - Pseudomonas aeruginosa
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A;Map position: 2
C;Superfamily: probable transporter MJ0672
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'CgnZ_6/ptodata1/iaa/PCTUS COMB.pep:*
'CgnZ_6/ptodata1/iaa/backfiles1.pep:*
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(c) 1993 - 2005 Compugen Ltd.
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Sequence 2, Appli
Sequence 9, Appli
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Sequence 250, Appli
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; Sequence 36, Application US/09912935
; Patent No. 6673904
; GENERAL INFORMATION:
; APPLICANT: Nishikawa, Mitsuo et al.
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STER
; TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
; FILE REFERENCE: 32066/37483
; CURRENT APPLICATION NUMBER: PCT/US/09/912,935
; CURRENT FILING DATE: 2001-07-24
; PRIOR FILING DATE: 2001-07-24
; PRIOR PLING DATE: 2000-12-23
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin version 3.0
; SSOFTWARE: Patentin version 3.0
  US-08-484-993B-18
US-08-484-158B-18
US-08-484-596A-18
US-08-480-150A-18
US-08-458-731-18
US-08-458-731-18
US-08-458-731-18
US-09-223A-18
US-09-232-991A-31114
US-09-248-796A-14652
US-09-248-796A-2
US-09-273-986-9
US-09-573-986-9
US-09-461-325-250
US-09-461-325-250
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US-09-912-935-36
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Best Local Similarity
Matches 416; Conserv
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Sequence 40, To Application US/09912935

Sequence 40, To Application US/09912935

Patent No. 6673904

GENERAL INFORMATION:

APPLICANT: Nishikawa, Mitsuo et al.

TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFERENCE: 32066/37483

CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT PILLING DATE: 2001-07-24

PRIOR APPLICATION NUMBER: PCT/US00/35260

PRIOR FILING DATE: 2000-12-23

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NOS: 53
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POLYPEPTIDES AND POLYNUCLEOTIDES
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48.1%; Score 1295; DB 4;
Best Local Similarity 57.3%; Pred. No. 1.7e-120;
Matches 250; Conservative 72; Mismatches 106;
                 FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
FRIOR PELION ADTE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
LENGTH: 529
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US-09-912-935-28
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TYPE: PRT
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                                                                                                                                                                                             Sequence 31, Application US/09912935

Patent No. 6673904

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
MITSURE INVENTION:
MITSURE OF INVENTION:
MITSURE OF INVENTION:
FITLE OF INVENTION:
FITLE FERENCE: 32066/37483

CURRENT PAPLICATION NUMBER: US/09/912,935

CURRENT PILION DATE: 2001-07-24

PRIOR APPLICATION NUMBER: PCT/US00/35260

PRIOR APPLICATION NUMBER: PCT/US00/35260

PRIOR SEQ ID NOS: 53

SOFTWARE: PatentIn version 3.0

SEQ ID NO 31

LENGTH: 499
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72 LAMDTLPDNRTRVVED-NHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHR 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 PVKVGLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEMTPLPTCLQFNRC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 DACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPD 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T--SFSPYDGDLTTTS---SSLFIDSLTTEDDTKLNPYAGGDGLQ-NNLSPKTKGTPVHL 424
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                                                            484 VEPSGHEKEGFMEAEQC 500
                                                                                        485 EPVG-EKEGFIVSEOC 499
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; ORGANISM: Homo sapiens
US-09-912-935-31
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US-09-912-935-28
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         DAFMILNPSPDVPESRRRSI FEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD
                         DAFVVVHRIQOIPNVRRRIIYEYHRVELQMSKIINISAVEMIPLPICLQFNRCGPCVSSQ
                                                                            VLAVLLVAAIILAGIYINGHPTSNAALFFIERRPHHWPAMKFRSHPDHSTYAEVEPSGHE
                                                                                                                                                                                       PTEDDTKIALHLKDSGASTDDSAAEKKGGTLHAGLIVGILILVLIIAAAILVTVXMYHHP
                                                              LTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCED-----FQDEDHDSASPDT
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                                                                                                                 SFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQ-NNLSPKTKGTPVHLGTIVGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 WNRRARESPGHVSEPDRTQLSQ----DLGGGTLAMDTLPDNRTRVVED-NHSYYVSRLYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 IFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYYFDNGTVFVVQWDHVYLQGWEDKGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.4%; Score 1275.5; DB 4; Length 530; 52.9%; Pred. No. 1.6e-118; ive 77; Mismatches 129; Indels 15;
                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NISHIKAWA, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STERTILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT PEDELICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR FILING DATE: 2000-12-23
FRIOR FILING DATE: 2000-12-3
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PATENTIN VETSION 3.0
SOFTWARE: PATENTIN VETSION 3.0
                                                                                                                                                                                                                                                                                                                       Sequence 38, Application US/09912935; Patent No. 6673904; GENERAL INFORMATION:
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Matches 248; Conservative
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416 KEGFIVSEQC 425
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US-09-912-935-38
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US-09-912-935-38
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Sequence 35, Application US/09912935

Patent No. 6673904

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYEBPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: POLYEBPTIDES AND POLYNUCLEOTIDES
FILE REPERENCE: 32066/37483

CURRENT FILIATION NUMBER: US/09/912,935

CURRENT FILIATION NUMBER: PCT/US00/35260

PRIOR APPLICATION NUMBER: PCT/US00/35260

PRIOR PILING DATE: 2000-12-23

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.0

SEQ ID NO 35

LENGTH: 425
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                                                                                                   QASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNS 190
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                                                                72 LAMDTLPDNRTRVVED-NHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHR
                                                                                                                                                         TVVYPDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQH
                                                                                                                                                                                                               PVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSC
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                      Gaps
                      8;
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57.7%; Pred. No. 9.7e-119;
ive 64; Mismatches 106; Indels
                     Indels
                     Mismatches 106;
         Pred. No. 1.7e-120;
57.3%; Pre-
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248; Conservative
                     Conservative
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; ORGANISM: Homo sapiens
US-09-912-935-35
        Similarity
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US-09-912-935-35
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y APPLICANT: Labat, Ivan

APPLICANT: Tang, Y. T.

APPLICANT: Tang, Y. T.

APPLICANT: Tang, Y. T.

APPLICANT: Tang, Y. T.

APPLICANT: Chids, Cheng-Chi

APPLICANT: Chids, John

TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell

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TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell

TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell

TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Methods and Materials and Methods and Method
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DB 4; Length 392;
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                                                                                                                                                                             Sequence 23, Application US/09764325A Patent No. 6667391
GENERAL INFORMATION;
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; Sequence 25, Application US/09764325A
; Patent No. 6667391
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ORGANISM: Homo sapiens
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US-09-764-325A-23
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Sequence 23, Application US/09912935
Sequence 23, Application US/09912935
Sequence 23, Application US/09912935
Sequence 23, Application US/0904
GRNERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPRESENCE: 3206/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION UNBER: PCT/US00/35260
PRIOR FILING DATE: 2000-112-23
NUMBER OF SEQ ID NOS: 53
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Tang, Y. T.
APPLICANT: Tang, Y. T.
APPLICANT: Tang, Y. T.
APPLICANT: Chids, Cheng-Chi
APPLICANT: Childs, John
TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides
TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides
TITLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides
TILE REFERENCE: 3026/37630A
CURRENT FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: 09/547,358
PRIOR APPLICATION NUMBER: 09/547,358
PRIOR PILING DATE: 2000-04-11
PRIOR PLING DATE: 2000-04-07
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NOS: 25
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43.7%; Score 1176.5; DB 4
Best Local Similarity 58.6%; Pred. No. 7.6e-109;
Matches 229; Conservative 60; Mismatches 95;
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APPLICANT: Nightkawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37443
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT PILING DATE: 2001-07-24
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 34
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                      296 VEPTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRM
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  KEIPMSVPEISSSOHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 34, Application US/09912935; Patent No. 6673904; GENERAL INFORMATION:
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US-09-912-935-34
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US-09-912-935-34
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US-09-181-706-2
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APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR FILING DATE: 2001-12-23
PRIOR FILING DATE: 2000-12-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 XDKVKIHGILSNTHRQAARVNLSFDPPFYGHFLREITVATGGFIYTGEVVHRMLTATQYI 62
                                                                                                                                                                                                                      116 RSQVKIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYV
                                                                                                                                                                                                                                                                                                   APLMANFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAY
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                                                                                                                                                                            7;
                                                                                                                                     43.7%; Score 1176.5; DB 4; Length 392; 58.6%; Pred. No. 7.6e-109; ive 60; Mismatches 95; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 43.7%; Score 1176.5; DB 4; Length 392; Best Local Similarity 58.6%; Pred. No. 7.6e-109; Matches 229; Conservative 60; Mismatches 95; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKFRSHPDHSTYAEVEPSGHEKEGFMEAEQC 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 25, Application US/09912935; Patent No. 6673904
SOFTWARE: Patentin version 3.0
SEQ ID NO 23
LENGTH: 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 53
SOFWARE: Patentin version 3.0
SEQ ID NO 25
LENGTH: 392
                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-09-912-935-25
                                                                             ; ORGANISM: Homo sapiens
US-09-912-935-23
                                                                                                                                                          al Similarity
229; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -09-912-935-25
                                                                                                                                       Query Match
Best Local S
Matches 229
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                                                          TYPE: PRT
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310 CDACMSSDLTFNCSWCHVLQRCSSGFDRYRQE----WMDYGCAQEAEGRMCEDFQ----D 361
                                                                                                                                                                                                                                                                                                                       APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
RECEPTOR DNA AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
4.3%; Score 115.5; DB 3;
Best Local Similarity 20.6%; Pred. No. 0.086;
Matches 77; Conservative 42; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/458,791
FILING DATE: 10-Dec-1999
CLASSIFICATION CATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/958,598
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-458-791-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631
                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1569 amino acids
                                                                                                                                                                                                                                                      Sequence 2, Application US/09458791
Patent No. 6174689
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS
                                                                                                                                        529
                                                                                             362 EDHDSASPDTSFSP 375
                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                            S16 KEKTTVTMVGSFSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: WA
COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 LILSSSLVEALDVWAGVFSAAAGEGÕERRSPITIALCIFRMSEIQARAKRVSWDFKTAES 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195 FDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    250 HPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTGLQHRS 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHRQASRVVLSF---- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 -----DPPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 HCKEGDOPERVOPIASSTL-----IHSDLTSV-YGTVVM------NRTVLF 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 GTVRGWNRRARESPGHVSEPDRT----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/958,598 (converted to a APPLICATION NUMBER: US 08/958,598 (converted to a APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION:
PRIOR APPLICATION NUMBER: --to be assigned-- (USSN 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING DATE: October 26, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION NUMBER: 34,347
FREEERENCE/DOCKET NUMBER: 2631-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.3%; Score 115.5; DB 3; Length 1568; 20.6%; Pred. No. 0.086; ive 42; Mismatches 118; Indels 137;
Sequence 2, Application US/09181706
Patent No. 6130068
GENERAL INFORMATION:
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Robert F. DuBose, Richard S. Johnson
TITLE OF INVENTION: VIRAL ENCODED SEMARHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/181,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: October 28, 1998 CLASSIFICATION:
                                                                                                                                                         NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acid
TYPE: amino acid
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Best Local Similarity 20.0-
Local 77; Conservative
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                                                                                                                                                                                                                                                      CITY:
STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----DFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353 HCKEGDOPERVOPIASSTL-----IHSDLTSV-YGTVVM-----NRTVLF 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 137;
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------BGQLLKVILGENLTSNCPEVIYEIKEE 422
                                                                                              423 TPV-----FYKLVPDP------VKNIXIY------LTAGKEVRIRVANCNKHKS 460
                                                                                                                                                                                    461 CSECLTA-TDPHCGWCHSLQRCTFQGDCVHSENLENWLDI----SSGAKKCPKIQIIRSS 515
                                                                                                                                                      310 CDACMSSDLTFNCSWCHVLQRCSSGFDRYRQE----WMDYGCAQEAEGRMCEDFQ----D 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHRQASRVVLSF---- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 LLISSSLVEALDVWAGVPSAAAGEGGERRSPTTTALCLFRMSEIQARAKRVSWDFKTAES 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 GTVRGWNRRARESPGHVSEPDRT----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVS 94
                                                                250 HPVKTGLSDAFMILNPSPDVPESRRRSIFBYHRIBLDPSKVTSMSAVEFTPLPTCLQHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Mismatches 118; Indels 137; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                256 GAATGWPSMAR----IAQSTEVLFQGQASLDCGHGH-----PDGR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Spriggs, Melanie
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
CORRESPONDENCE: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 4.3%; Score 115.5; DB
Best Local Similarity 20.6%; Pred. No. 0.086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: MS-DOS/Windows 95
Word for Windows 95, 7.0a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word for Windows 95, 7. (CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/459,065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09459065
Patent No. 6562949
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS/Wir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                            362 EDHDSASPDTSFSP 375
                                                                                                                                                                                                                                                                          516 KEKTTVTMVGSFSP 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (206)470-4189
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1568 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-09-459-065-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
3Y: linear
                       392 LGTG----
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250 HPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRS 309
                                         423 TPV-----FYKLVPDF-----VKNIYIY------LTAGKEVRRIRVANCNKHKS 460
                                                                                     CDACMSSDLTFNCSWCHVLQRCSSGFDRYRQE----WMDYGCAQEAEGRMCEDFQ----D 361
                                                                                                               GAATGWPSMAR-----IAQSTEVLFQGQASLDCGHGH------PDGR------R 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LSNTHRQASRVVLSF---- 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    293 LILSSSIVEALDVWAGVFSAAAGEGGERRSPTTTALCLFRMSEIQARAKRVSWDFKTAES 352
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------NRTVLF 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 GTVRGWNRRARESPGHVSEPDRT----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVS 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 1568;
                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09459066
; Patent No. 6187909
; GENERAL INFORMATION:
; APPLICANT: Spridge, Melanie
; TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             353 HCKEGDQPERVQPIASSTL-----IHSDLTSV-YGTVVM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.3%; Score 115.5; DB 3;
20.6%; Pred. No. 0.086;
iive 42; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS-DOS/Windows 95
SOFTWARE: Word for Windows 95, 7.0a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/459,066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/958,598
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 26.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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516 KEKTTVTMVGSFSP 529
                                                                                                                                                                         362 EDHDSASPDTSFSP 375
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TYPE: amino acid
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Best Local Similarity 20.6
Matches 77; Conservative
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US-09-459-066-2
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STATE: WA
COUNTRY: US
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353 HCKEGDQPERVQPIASSTLIHSDLTSV-YGTVVMNRTVLF 391	195 FDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPWSVPEISSSQ 249	392 LGTG	HRIELDPSKVTSMSAVEFTPLPTC	423 TPVPYKLVPDPVKNIYIYLTAGKBVRRIRVANCNKHKS 460	310 CDACMSSDLTFNCSWCHVLQRCSSGFDRYRQFWMDYGCAQEAEGRMCEDFQD 361	461 CSECLTA-TDPHCGWCHSLQRCTFQGDCVHSENLENWLDISSGAKKCPKIQIIRSS 515	362 EDHDSASPDTSFSP 375	S16 KEKTTUTMVGSFSP 529
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Search completed: January 28, 2005, 22:14:18 Job time : 42.8779 secs

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                 - protein search, using sw model
              Copyright
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January 28, 2005, 21:55:58; Search time 34.626 Seconds (without alignments) 1389.370 Million cell updates/sec Run on:

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1 MRGELWLLVLVLREAARALS......YAEVEPSGHEKEGFMEAEQC 500 US-09-918-715-230 2691 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 200000000 Minimum I Maximum I

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

<b>70</b>	Description	hypothetical prote	nidogen precursor	semaphorin recepto	probable cellulose	EH domain protein	hypothetical prote	phosphoenolpyruvat	hypothetical prote		probable membrane	NEDD-4 ORF - mouse	corticosteroid-bin	hypothetical prote	homeotic protein H	ubiquitin ligase N	alpha tectorin - c	neprilysin (EC 3.4	protein-tyrosine-p	PTP 35 protein - m	sodium channel alp	Ę	IFH1 protein - yea	pectate lyase (EC	probable receptor	hypothetical prote	a]	2a protein - broad	mucin 5AC (clone L
SUMMARIES	Ω	T19786	S31213	T09074	C86446	T09173	E86345	S18606	T12529	T16074	S45429	183196	S33415	T19703	S71480	S70642	T30243	JC7265	JC2349	148721	S54771	AG3506	855352	JC7653	A85041	A98241	F86088	P2WMBB	A57534
	DB	~	7	7	~	7	7	7	~	~	N	~	7	7	-	~	~	N	Н	~	~	7	0	7	N	N	~	-1	7
	Length	476	1161	1568	979	743	733	535	1133	345	1502	708	397	619	399	887	2120	774	979	966	1977	491	1085	441	852	614	614	810	1042
d	Query Match	22.7	4.7	4.3	3.8	3.8	3.8	3.7	3.7	3.6	3.6	3.6	3.6	3.6	3.5			3.5	3.5	3.5	3.5	3.5	3.5	3.4	3.4	3.4	3.4	3.4	3.4
	Score	611	126	115.5	103.5	101.5	101	100	66	96	98	97	96.5	96.5	95.5	95.5	95.5	94	93.5	93.5	93.5	93	93	92.5	92.5	91.5	91.5	91.5	91.5
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protein-tyrosine-p pregnancy-specific	zona periucida giy pristinamycin I sy phosphoenolpyruvat	phosphoenolpyruvat hypothetical prote protein tyrosine p	hypothetical prote hypothetical prote protein-tyrosine k	Doc4 protein, stre pregnancy-specific osteonidosen - bum	probable polyketid sodium channel pro
S51005 JN0067	S70399 T30289 AD2581	B97363 T25104 I58345	T05673 T51491 T30200	T14271 A34595 G00043	T03222 CHRTM1
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## ALIGNMENTS

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A;Cross-references: UNIPROT:Q18500; EMBL:Z35597; PIDN:CAA84646.1; GSPDB:GN00021; CESP:C3
A;Experimental source: clone C36E8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46 RRARESPGHVSEPDRTQLS-----QDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPS 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 GSFTFQAALHHDGRIVFAYKEIPMSVPEISSSOHPVKTGLSDAFMILN--PSPDVPESRR 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLT-FNCSWCHVLQR--- 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 SSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTIVGIVLAVLLVAAIILAG 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDK 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 HSFTFQTILHKNGDIVFIYKDVPYDISNISDANHPVKLGISDAYMFKHNLHQAAVP---K 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -- CS--SGFDRYRQEWMDYGCAQEAEGRMCE-DFQDEDHDSAS-PDTSFSPYDGDLTTTS 384
                            C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C.Accession: T19786 R.Wilkinson, J.; Barlow, K. submitted to the EMBL Data Library, August 1994 A.Reference number: Z19177 A.Reference number: Z19177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 EPHSRELWVDVAEANRSOVKI----HTILSNTHROASRVVLSFDFPFYGHPLROITIATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
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A;Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2
C;Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3
                                                                                                                                                                                                                                                                                                                                                                                              Query Match

22.7%; Score 611; DB 2; Length 476;
Best Local Similarity 34.2%; Pred. No. 5.6e-42;
Matches 149; Conservative 65; Mismatches 160; Indels
lypothetical protein C36E8.3 - Caenorhabditis elegans
                                                                                                                                                               A)Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-476 <WIL>
                     C; Species: Caenorhabditis elegans
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362 EDHDSASPDTSFSP 375
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Matches 77; Conserv
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                                                                                                                                                                                                                                                                                                  Jail Descursor - sea squirt (Halocynthia roretzi)

N.Alternate names: entactin
C,Species: Halocynthia roretzi
C,Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C,Accession: 531213
R,Nakae, H.; Sugano, M.; Ishimori, Y.; Endo, T.; Obinata, T.
Bur. J. Blochem. 213. 11-19, 1993
A,Title: Ascidian entactin/nidogen. Implication of evolution by shuffling two kinds of A;Reference number: 531213; MUID:9328676; PMID:8477687
A,Accession: 831213
A,Molecule type: mRNA
A,Reference number: 531213; MUID:9328676; PMID:8477687
A,Cross-references: UNIPROT:Q04901; EMBL:D14038; NID:g217363; PIDN:BAA03127.1; PID:g2173
C,Superfamily: Ascidian midogen; EGP homology; LDL receptor YMTD-containing repeat homology (S,Keywords: basement membrane; collagen binding; disulfide bond; duplication; extracellu C,Keywords: basement membrane; collagen binding; disulfide bond; duplication; extracellu C,Keywords: basement membrane; medicted <NGS
C,Superfamily: Ascidian midogen #status predicted <NGS
C,Keywords: basement membrane; mollogen #status predicted <NGS
C,Keywords: basement membrane; repeate (MTS)
F;20-1161/Product: nidogen #status predicted <NGS
F;21-1161/Product: nidogen #status predicted <NGS
F;21-20/Domain: thyroglobulin type I repeat homology <THYS)
F;60-673/Domain: thyroglobulin type I repeat homology <THYS)
F;90-943/Domain: LDL receptor YMTD-containing repeat homology <YW3>
F;90-943/Domain: LDL receptor YWTD-containing repeat homology <W3>
F;102-1075/Domain: LDL receptor YWTD-containing repeat homology <W3>
F;102-1114/Domain: LDL receptor YWTD-containing repeat homology <W3>
F;102-1118/Domain: LDL receptor YWTD-containing repeat homology <W3>
F;102-1075/Obmain: LDL receptor YWTD-containing repeat homology <W3>
F;102-1075/Obmain: LDL receptor YWTD-containing repeat homology <W3>
F;100-1054/Obmain: LDL recepto
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Affille: A poxvirus-encoded semaphorin induces cytokine production from monocytes and kakeference number: 216555; MUID:98246049; PMID:9586637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;107,334,360,484/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --FNPGYSDNSTVVY------PDNGTVFVVQWDHVYLQGWEDKGSFTFQAA 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LHHDGRIVFA---YKEIPMSVPEIS----SSQHPVKTGLSDA----FMILNPSP----DV 269
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C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09074
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23.5%; Pred. No. 0.094;
iive 34; Mismatches 8
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458
                                                                   445 IYINGHP--TSNAALF
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1568 <CON>
A;Residues: 1-1568 <CON>
A;Cross-references: UNIPROT:060486; EMBL:AF030339; NID:g3176761; PIDN:AAC18823.1; PID:g3
A;Experimental source: tissue type foreskin; cell type fibroblast
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ansen, N.F.; Hughes, B.; Huizar, L.
Asture 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, J.H.; Li, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353 HCKEGDOPERVOPIASSTL-----IHSDLTSV-YGTVVM-----NRTVLF 391
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C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                       Length 1568;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                             20.6%; Pred. No. 1,
tive 42; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
3.8%; Score 103.5; D
Best Local Similarity 21.2%; Pred. No. 5.2;
Matches 87; Conservative 48; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                               4.3%; Score 115.5;
                                                                                                                                                                                                                                                              A,Gene: VESPR
C,Keywords: receptor; signal transduction
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q	342 EKWKHWKVKVEEDQIKEPRPALVAPKATWMSDGTHWPGTWAVSGPHHSRGDHASV 396	QY 267 PDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCH 326
è 8	64 SQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSR 105	327 VLORCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDTS
& 8	106 ELWVDVAEANRSQVKIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVI 165	Db 362 LNGSSEQWETFS-ERSSSSQTLTQF-DSNIAPADPDTAIVHPVPIRMTPSKI 411 Qy 373FSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLS 414
ठे व	HRMLTATQYNAPLMANFNPGYSDNSTVVY-F	Db 412 HMQEMELKRISSDHINPISPLLVKPSDLSEENKINSSVKFPSGNTVDGYSSSDSFPSD 469 Qy 415 PKTKGTPVHLGT 426
8 & 8	494 GDRVSYVQFPQRFEGIDPSDRYANKNIVFFDINLRALDGIQGFMYVGTGCLFRRTALYGF 553 196 DNGTVFVVQWDHVYLQGWFDKGSFTFQAALHHDGRIVFAYKEIPMSVPRISSSQHP- 251	Db 470 PEQIGSSVTRQRSHSGT 486
qa	:         : : :         :         :	RESULT 6
දු පු	252VKTGLSDAFMILNPSPDVPESRRRSIFEYHRIBLDPSKVT-SMSAVEFTPLPT 303 :   :	hypothetical protein F16F4.9 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
<u>ک</u> ۾	304 CLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAE 352 :	C;Accession: E86345 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hudhes, B.; Huizar, L.
RESULT 5		Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
T09173 EH domain		Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, O.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ber M. W. N. O. V. G. France C. M. Venter J. C. Davie, P. W.
C; Species C; Date: 1	ange 09-Jul-2004	Aritie: Sequence and analysis of chromosome I of the plant Arabidopsis. A; Title: Sequence and analysis of chromosome I of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712
C; Access: R; Yamaguc J. Biol. A; Title:	the ral-GTPase target, RalBP1	A;Accession: accident
A; Referer A; Accessi A; Status:		A;cros-references: UNIPROT:Q9LMN7; GB:AE005172; NID:g8920637; PIDN:AAF81359.1; GSFDB:GN. C;Genetics: A;Map position: 1
A; Molecu. A; Residut A; Cross-1 A; Experin	916; EMBL:AF031939; NID:G2677842; PIDN:AAB94736.1; PID:G2 e: C2C12; Lissue Lype: muscle	C;Superfamily: Arabidopsis probable serine/threonine-specific protein Kinase PR025; prot Query Match 3.8%; Score 101; DB 2; Length 733; Best Local Similarity 24.1%; Pred, No. 5.5;
A;Genera	cs: reps1	Macciles 55; conservative 24; mismarciles 72; illusts 50; caps
C; Keywork	i: signal transduction	QY 257 SDAFMINDSPDVPESRRRSIFEYHRIELDPSKVTSMSAVE-FTPLPTCL 305  Dh
Best Loc Matches	al Similarity 18.3%; Prod. No. 5.1; 91; Conservative 63; Mismatches 166; Indels 1	306 QHRSCD-ACMSSDLTFNCSSS
È	19 LSPQPGAGH-DEGPGSGWAAKGTVRGWNRRARESPGHV 55	DD 194CSYAFFVEDGMFNFSSLEDLKDLRNVTRFPVLLDWSIGNQTCEQVVGRNICGGNST 249
qo ,	I PPPPPGRQVKKGPGSHDAVQPRPSAEQQEPASPVVSPQQSPPTSPHTWRKHSRHPSGGN	334 GFDRYRQEWMDYGCAQBAEGRMCEDFQDEDHDSASPDTSFSPY
충 음	Se SEPDRIQUESQ DIGAGILAMOTINDENTIKVVEDNHSIXVSKLYGEPERHSKELWV 109  138 SERPLTGPGPFWSPFGDAQAGSAGDAVWSGQSPPPPQDNWV 179	DD 250 CFDSTRGRGTNCRCLGGFDGNFILSDGCQDINECITRIANCSDISTCENILGSFACGCFS 309 Qy 377 DGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKG-TPVHLGTIVGIVLAVL 435
È	DVAEANRSQVKIHTILS-NTHRQASRVVLSFDFPFYGHPLRQITIAT	310
a	180 SPADTPPTSALLTMHPASVQDQTTVRTVASAATANEIRRQSSSYEDPWKITDE- 232	Oy 436 LVAAI 440
ð i	GGPIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDNGTVFVVQWDHVY-LQG	Db 350 Ti8Yi 354
8 è	233QRQYYVNQFKTIQPDLNGFIPGSAAKEFFTKSKLPILELSHIWELSD 279 213 WEDKGSPTFOAALHHDGRIVFAYKEIPMSVPEISSSOHPVKTGLSDAFMILNPS 266	RESULT 7 S18606
: 음	:  :	phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - Rhizobium sp. C;Species: Rhizobium sp. C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 27-Oct-2003

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Mosidues: 1-345 <GET-
A;Kesidues: 1-345 <GET-
A;Cross-references: UNIPROT: Q19446; EMBL: U28737; NID: G860717; PID: G860723; PIDN: AAA68276
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nyllearnate ammens: hypothetical protein YBL0725
C;Species: Saccharomyces cerevisiae
Sycoension: S45429; S45820; S45815; S5226
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
Submitted to the EMBL Data Library, May 1994
A;Description: Sequence analysis of a 78,6 kb segment of the left end of Saccaromyces ceals. A;Reference number: S45387
A;Accession: S45429
A;Accession: S45429
A;Accession: S45420
A;Cross-references: UNIPROT: P38181; EMBL:X79489; NID:G496661; PID:G496702
                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 PLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDF 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDEDHDSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----GDVNPD-DCSYYDHPISTTWSP---------NTQCSASAEN 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPVHLGTIVGIVLAVLLVAAIIL-----AGIY------INGHPTSNAALFF 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 TYFWLMISFAIIIAILLAILLLULLELCCGLFTGRQSARRSEDGDWIVPKTPKANHELYD 282
  AFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTC-LQHRSCDACMSSD 317
                                                                                                             318 LIFNCSWCHVLORCSSGFDRYRQEWMDYGC------AQEAEGRMCEDFQDEDH 364
                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein F14B8.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T16074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                146 LTATI --NRKCNG--ADQYGFNCN----EQCST----VNNDYYCYTCGSNGQKTCCAS-
                                                      937 AMLOADDEDDLMEERMKSPF-----GSSFRTFNATDYKPIATIDVKRNIFDLCTD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 MSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                          16;
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                                                                                                                                                                                                                        365 DSASPDISFSPYDGDLTIISSSLFIDSLTIEDDIKLNPYAGGDGLQNNLSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Introns: 17/3; 61/2; 93/3; 144/2; 197/1; 218/3; 255/2; 327/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R,Geisel, C. submitted to the EMBL Data Library, June 1995 A;Description: The sequence of C. elegans cosmid F14B8. A;Reference number: Z18456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
3.6%; Score 98; DB 2
Best Local Similarity 18.7%; Pred. No. 3.4;
Matches 50; Conservative 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      460 IERRPHHWPAMKFRSHPDHSTYAEVEP 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADITPHH---OYRRHODNNSGESTEP 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP: F14B8.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: T16074
                                                                                                                                                                                                                                                                                  1041
     259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Genetics:
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                                                                                      encodin
                                                                                   pckA of Rhizobium NGR234,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 ----DKGSFTFQAALHHDGRIVFAYKEI------PMSVPEISSSQ---HPVKTGLSD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               877 AIHKEDKFNMNISGVFHPNGLEVIINTEIWDLRTFHLLHTVPALDQCRVVFNHTGTVMYG 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTLAMDT----LPDNRTRVVED-----NHSYYVSRLYGPSEPHSRELWVDVAEANRSQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDQIWWDNNSAISPENFERLRQDMLAHAKGMSLYVQDLVGAGQSGK-----CVADARRHR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 VKIHTI-LSNTHRQASRVVLS-----FDFP-FYGHP-------LRQITIA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 IRWHSLFIRNLLIRPPREGLASFLPKLTIIDLPSFKANPERHGCRGETIIACDLTKGLVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -DNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKT 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 VLREAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHV--SEPDRTQLSQDLG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 VERPLGRSLQLRAABLYEE----AFARRGALTAHGALCARTGQHTGRSPKDKYVVRDAAT 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 GLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTFLPTCLQHRSCDA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 VMENVVLDERRAPDFDNG---SLTENTRIAYPLDFIPNASETGTAPOPRTIIMLTADA 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ri2529
hypothetical protein DKFZp434P113.1 - human (fragment)
hypothetical protein DKFZp434P113.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 23-Uul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C;Accession: T1529
R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z17524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDIAH -- IYDIQTGNKLLTLFNPDLANN -- -- YKRNCATFNPTDDLVLNDGVLWDVRSAQ
                                                                                                                                                                                                                                                     A,Cross-references: EMBL:X63291
C,Superfamily: phosphoenolpyruvate carboxykinase [ATP]
C,Keywords: carbon-carbon lyaes; carboxy-lyaes; nucleotide binding; P-loop
F;234-241/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         80;
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                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 535;
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                                                                                                                                                                                                                                                                                                                                                                                            3.7%; Score 100; DB 2; Length 53:
19.8%; Pred. No. 4.3;
tive 50; Mismatches 157; Indels
C;Accession: S18606
R;Osteras, W.; Finan, T.M.; Stanley, J.
Mol. Gen. Gene. 230, 257-269, 1991
A;Title: Site-directed mutagenesis and DNA sequence of p
A;Reference number: S18606; MUID:92079905; PMID:1720862
A;Accession: S18606
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-535 <OST>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: T12529
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1133 «WAM»
A;Cross-references: UNIPROT:Q9UG37; EMBL:AL080145
A;Experimental source: adult testis; clone DKFZp434P113
A;Note: DKFZp434P113.1
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 19.00
-ham 71; Conservative
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Best Local Similarity
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Query Match
Best Local Similarity
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                                                                                                 1-708 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 EPD----
                                                                                                                                                                       A; Gene: NEDD-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268
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                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1262-1502 <CON>
A;Cross-references: EMBL:235840; MIPS:YBL079w
A;Experimental source: strain S288C
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
A;Title: Sequence analysis of a 78.6 kb segment of the left end of Saccharomyces cerevis
A;Reference number: S59184; MUID:96076635; PMID:7502586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183196 --
NEDD-4 ORF - mouse (fragment)
C;Species 102-Aug-1996 #text_change 18-Aug-2000
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
C;Accession: 183196
R;Kumar, S.; Tomooka, Y.; Noda, M.
Biochem: Biophys. Res. Commun. 185, 1155-1161, 1992
A;Title: Identification of a set of genes with developmentally down-regulated expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:X79489; NID:g496661; PIDN:CAA56029.1; PID:g496702
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 IHTILSNTHRQASRVVLSFD-FPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAP-L 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRLLRDIWGRHVFM-TFTDNRV----TSHAFISSS--DPITPSINNLKSDEISQNRNII- 829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MANFNPGYSDNSTVVYFD-----NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LANNSNGRVIDKTEEVANQAESIAINAMIKMVQ-----SIKEGLSFLNVLYEESEV 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIEL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   920 EGFDNQYLGFKDI-ISFVSLDVQKDLVKLDFKDLF-----APNDKTKSLIREILLSI 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
A; Experimental source: strain S288C

R; Domdey, H; Gaseenhuber, H; Obermaier, B.; Piravandi, E.

submitted to the Protein Sequence Database, August 1994

A; Reference number: 845816

A; Accession: 845820

A; Molecule type: DNA

A; Residues: 1-1502 < DOM>

A; Cross-references: EMBL: 235840; NID: 9536126; PID: 9536127; MIPS: YBL079w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-1502 <OBW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.6%; Score 98; DB 2; Length 1502; Best Local Similarity 22.7%; Pred. No. 26; Matches 62; Conservative 41; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;231-247/Domain: transmembrane #status predicted <TM1>F;434-450/Domain: transmembrane #status predicted <TM2>F;764-780/Domain: transmembrane #status predicted <TM3>F;1311-1327/Domain: transmembrane #status predicted <TM4>F;13182-1399/Domain: transmembrane #status predicted <TM4>F;1382-1399/Domain: transmembrane #status predicted <TM5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1406-1423/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                         A; Experimental source: strain S288C
R; Contreras, R.; Fiers, W.; Logghe, M.; Molemans, F.
submitted to the Protein Sequence Database, August 1994
A; Reference number: S45802
A; Accession: S45815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDL 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: SGD:S0000175; MIPS:YBL079w A; Map position: 2L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Keywords: nucleus; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: SGD:NUP170
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C;Superfamily: rat ubiquitin-protein ligase; protein kinase C C2 region homology; ubiquiti9-77/Domain: WW repeat homology <WW1>
F;196-237/Domain: WW repeat homology <WW2>
F;251-288/Domain: WW repeat homology <WW3>
F;251-288/Domain: WP repeat homology <WW3>
F;347-682/Domain: ubiquitin-protein ligase homology <UBI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corticosteroid-binding globulin precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: 833415; 843740
R;Scrocchi, L.A.; Orava, M.; Smith, C.L.; Han, V.K.M.; Hammond, G.L.
Ascission: Spatial and temporal distribution of corticosteroid-binding globulin and its me A;Reference number: S33415; MUID:93145908; PMID:7916682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-397 <SCR1>
A;Cross-references: UNIPROT:Q06770; EMBL:X70533; NID:g298114; PIDN:CAA49934.1; PID:g2981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              232 VFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESR-RRSIFEYHRIELDPSKV 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQE 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 AEGRMCEDFQDE---DHDSASPD-----TSFSPYDGDLTTTSSSLFIDSLTTEDDTKL 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       347 LKARLWIEFDGEKGLDYGGVAREWFFLISKEMFNPYYG------LFEYSATDNYTLQI 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 SPDDDLTDEDNDDMQLQAQRAFTTRRQISEDVDG-----PDNRESPENWEIVREDEN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYYVSR-LYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLSFDF----PFY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 TEYSGQAVQSPPSGH----IDV-----IDV------QTH------IAEFFNTRLAVC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLM----ANFNPGY----SDNSTVVYFD 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 GNPATSQPVTSSNHSSRGGSLQTCIFEEQPTLPVLLPTSSGLPPGWEEKQDDRGRSYYVD 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 HNSK-TTTWSKPTMQDDPRSKIPAHLRGKTDSNDLGPLPPGWEER-----THTDGRV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ------LRRANILEDSYRR-IMGVKRADL 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197 NGTVFVVQWDHVYLQ----------GWEDKGSFTFQAALHHDGRI 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 EAARALSP-----QPGAG----HDEGPG---SGWAAKGTVRG----WNRRARESPGHVS 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --RIQLSQDLGGGTLAMDTLPDNRTR-----VVEDNH 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOAEBLEPGWVVLDQPDAATHLPHPPEPSPLPPGWEBRQDVLGRTYYVNHESRRTQWKRP 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 708;
A; Reference number: 160167; MUID:92328780; PMID:1378265
                                                                                                                                                                                                             A; Cross-references: GB: D10714; NID: g220508; PID: g220509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51; Mismatches 154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.6%; Score 97; DB 2;
19.4%; Pred. No. 11;
                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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C;Superfamily: Serpin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S43740
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C; Keywords: glycoprotein; steroid binding F;1-22/Domain: signal sequence #status predicted <sig> F;23-397/Product: corricosteroid-binding globulin #status experimental <mat> F;89,169,217,232,253,320/Binding site: carbohydrate (Asn) (covalent) #status predicted</mat></sig>	QY 302 P 302   1 Db 586 P 586
Query Match 3.6%; Score 96.5; DB 2; Length 397; Best Local Similarity 20.2%; Pred. No. 5.5; Matches 53; Conservative 47; Mismatches 104; Indels 59; Gaps 11;	
Qy 61 TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEA 114      :	nomeotic procein hox bs - chicken C;Species: Gallus gallus (chicken) C;Becies: 0.5ep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C:Accession: S7480
115 NRSQVKIHTILSNTHRQASRVVLSFDFPPYGHPLRQITIATGGFIFMGDVIHR	R.Scotting, P.J.; Rex, M. submitted to the EMBL Data Library, August 1993 A.Reference number: S71480
DD 169 NKTGGKIEHVVSDLDSSATLILINYIFLKGIMKLPFSPENIKEEDFYV 216  QY 168 MLTATQYVAPLMANPNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFT 220  L	A,Accession: S71480 A,Status: preliminary A,Nolecule type: mRNA A,Residues: 1-399 - SCO> A,Accession: 1-399 - ACCO> A,Accession: 1-399 - ACCO> A,Accession: ACCO> A,A
21 FORALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNPSFDV 269 VVAALNRDTIDRWGKLMIP-RQMNLYIPKFSMSDTYDLQDVLADVGIKDLFTNQSDFADT	C.Genetics: Ontrolless: Ontrolless: Ontrolless: Ontrolless: Ontrolless: Ontrolless: Ontrolless: Ontrolless: A.Genetics: A.Genetics: A.Genetics: Ontrolless: Ontrol
Qy 270 PESRRSIFEYHRIELDPSKV 290  1 :     :          28 TKDTPLILTVLHKAMLQLDEGNV 350	Query Match 3.5%; Score 95.5; DB 1; Length 399; Best Local Similarity 20.5%; Pred. No. 6.7; Matches 62; Conservative 40; Mismatches 110; Indels 91; Gaps 10;
RESULT 13	QY 246 SSSQHPVKTGLSDAFMILNPSPDVPBSRRRSIFEYHRIELDPSKVTSMSAVEFT 299
hypothetical protein C34C12.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 09-Jul-2004	Db 94 ŚTŚSNSIPSGSAKVPRVKPTŚVQTP-ŚLTKQİFPWMKESRQNŚKQKŚSŚPSTETCSGEKT 152 Qy 300 PLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWM 343
	Db 153 PPGSSASKRARTAYTSAQLVELEKEFHFNRYLCRPRRVEMANLIALSERQIKIWFQNRRM 212
submitted to the EMBL Data Library, December 1994 A;Reference number: 219166 A;Accession: T19703	344 DYGCAQEAEGRMCEDFQDEDHDSASPDTSFSPYDGDLTTTSSSLFIDSLTT
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Resiques: 1-679 <wil></wil>	DD 213 KYKKDQKSKGMGSSSGGPSPTGSPPQPMQSSAGFMNALHIMSSNYDAPSPPS 264 OV 395 EDDTYLNPYAGGDGLONNLSPKTKGTPVHLGT 426
A;Cross-references: UNIPROT:Q09495; EMBL:Z46996; PIDN:CAA87102.1; GSPDB:GN00021; CESP:C3 A;Experimental source: clone C34C12	:
Cjeenerics: Ajgene: CSSP:C34C12.2 A.Man nord+ion: 4	Qy 427 IVGIVLAVLLVAAIILAGIYINGHPTSNAALFFIERRPHHWPAMKFRSHPDHSTYAEVEP 486
Ajmap position: 3 A;Introns: 5/3; 72/3; 125/3; 173/3; 511/3; 605/3	SLPTSGPSLYGLNHLPHHQAANMDYSGPP
Query Match 3.6%; Score 96.5; DB 2; Length 679; Best Local Similarity 23.3%; Pred. No. 12; Matches 70; Conservative 36; Mismatches 130; Indels 65; Gaps 12;	Oy 487 SGH 489 Db 362 SQH 364
OY 16 ARALSPOPCAGHDEGPGSGWAAKGTVRGWNRRARESPGHYSEPDRTOLSODLGGGTLAMD 75  1	RESULT 15 Synd42 ubiquitin ligase Nedd4 - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Species: 15, 2371-2380, 1996 R;Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D. R;Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D. R;Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D. R;Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D. R;Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D. A;Tile: www domains of Nedd4 bind to the proline-rich PY motifs in the epithelial Na(+) A;Accession: S70642 A;Status: preliminary; nucleic acid sequence not shown A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRNA A;Molecule type: mRNA A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics: A;Generics:

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149 RQITIATGGFIFMGDVIHRMLTATQYVAPLM----ANFNPGY----SDNSTVVYFDNGTV 200
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                                                                                                                                                                                                                                                                                                   48 ARES------PGHVSEPDRTQLSQDLGGGTLAMDTLPDNRTR-----VVEDNH 89
                                                                                                                           Query Match 3.5%; Score 95.5; DB 2; Length 887; Best Local Similarity 19.2%; Pred. No. 20; Matches 93; Conservative 55; Mismatches 155; Indels 181;
F;54-167/Domain: protein kinase C C2 region homology «KC2» F;246-239/Domain: WW repeat homology «WW1» F;402-439/Domain: WW repeat homology «WW3» F;459-496/Domain: Ww repeat homology «WW3» F;555-881/Domain: ubiquitin-protein ligase homology «UBI»
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2: /cgn2_6/ptodata/1/pubpaa/Der_Maw PuB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Sequence 230, App	Sequence 79, Appl			Sequence 179, App			Sequence 5, Appli		N	, ,	Sequence 192, App	Sequence 297, App
ID	US-09-918-715-230	US-10-435-696-79	US-10-474-794-230	US-10-357-819-2	US-09-918-715-179	US-10-474-794-179	US-10-357-819-4	US-10-156-487A-5	US-09-918-715-192	US-09-918-715-297	US-10-156-487A-6	US-10-474-794-192	US-10-474-794-297
88	101	15	17	17	10	17	11	14	10	10	14	17	11
% Query Match Length	500	. 500	200	200	1002	1002	488	502	200	200	200	200	200
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	7.96	95.4	82.1	82.1	82.1	82.1	82.1
Score	2691	2691	2691	2691	2691	2691	2602	2566	2209	2209	2209	2209	2209
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US-09-912-935-36 US-10-168-365-36 US-09-912-935-31 US-10-168-365-31 US-09-918-715-189	09-912 09-912 10-156 10-168	US-10-474-794-200 US-10-052-586-472 US-10-066-500-128 US-10-174-590-472 US-10-176-758-472	10-175-75-7-1 10-176-481-4 10-176-749-4 10-176-914-4 10-176-915-7 10-173-706-4 10-175-738-4	175-7 -175-7 -176-9 -176-9 -180-5 -173-5
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	MSGULT 1.  WESULT 1.  WESULT 1.  Sequence 230, Application US/09918715  Sequence 230, Application US/09918715  Sequence 230, Application No. US20030017157A1  GENERAL INFORMATION:  APPLICANT: Bart Vogelstein  APPLICANT: Bert Vogelstein  APPLICANT: Bert Vogelstein  APPLICANT: Trib.  APPLICANT: Bert Vogelstein  APPLICANT: MINOTHELIAL CELL EXPRESSION PATTERNS  FILE REFERENCE: 1107.00134  CURRENT APPLICATION NUMBER: US/09/918,715  CURRENT APPLICATION NUMBER: 60/224,360  PRIOR APPLICATION NUMBER: 60/224,360  PRIOR PLING DATE: 2000-08-11  PRIOR PLING DATE: 2000-08-11  PRIOR FILING DATE: 2000-08-11  PRIOR FILING DATE: 2000-08-11  PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR	100.0%; Score 2691; DB 10; Length 500; 100.0%; Pred. No. 4.9e-249; vative 0; Mismatches 0; Indels 0;	1 MRGELWLLVLVLREAARALSPQPCAGHDEGPGSGWAAKGTVRGWNRRARESPCHVSEPDR 	YVSRLYGPSEPHSRELM

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                                                           SVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTP
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US-10-474-794-230
Sequence 230, Application US/10474794
Publication No. US20040213793A1
Publication No. US20040213793A1

GENERAL UNPORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
APPLICANT: Winzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-01
PRIOR FILING DATE: 2001-04-01
SPRIOR FILING DATE: 2001-08-01
SEQ ID NO 230
LENGTHA: 500
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Best Local Similarity 100.0
Matches 500; Conservative
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APPLICANT: Wirtz, Ralph
APPLICANT: Minnes, Marc
APPLICANT: Minnes, Marc
APPLICANT: Minnes, Marc
APPLICANT: Minnes, Marc
APPLICANT: Minnes, Marc
TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA
FILE REFERENCE: LeA 36 108
CURRENT APPLICATION NUMBER: US10/435,696
CURRENT APPLICATION NUMBER: EP0303112.4
PRIOR FILING DATE: 2003-05-03
PRIOR FILING DATE: 2003-05-03
PRIOR FILING DATE: 2003-05-03
NUMBER OF SEQ ID NOS: 314
SOFTWARE: Patentin version 3.1
LENGTH: 500
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                                         IHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMA 180
                                                               SVPEISSSOHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVETP 300
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   TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
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US-10-435-696-79

Sequence 79, Application US/10435696

Publication No. US20040018525A1
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US-10-435-696-79
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                                                                                             1 MRGELWLLVLVLREAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDR
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100.0%; Score 2691; DB 10; Length 1002;
Best Local Similarity 100.0%; Pred. No. 1.4e-248;
Matches 500; Conservative 0; Mismatches 0; Indels 0;
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Length 500;
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100.0%; Score 2691; DB 17;
llarity 100.0%; Pred. No. 4.9e-249;
Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
US-09-918-715-179
                        Best Local Similarity
Matches 500, Conserv
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APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Shenoy, Mai
TILE REPERENCE: 21402-538A
CURRENT APPLICATION NUMBER: US/10/357,819
CURRENT APPLICATION NUMBER: 09/520,781
PRIOR APPLICATION NUMBER: 09/520,781
PRIOR APPLICATION NUMBER: 09/534,411
PRIOR PILING DATE: 2000-05-31
PRIOR PILING DATE: 2000-05-31
PRIOR PILING DATE: 2001-02-14
PRIOR PILING DATE: 2002-02-25
PRIOR PILING DATE: 2002-02-25
PRIOR PILING DATE: 2002-02-12
PRIOR PILING DATE: 2002-02-12
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    LPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQ 360
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NUMBER OF SEQ ID NOS: 142
SOFTWARE: CuraSeqList version 0.1
                                                                                                                                                                                                                                                                                  YAEVEPSGHEKEGFMEAEQC 500
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Miler, Charles E.
Padigaru, Muralidhara
Patturajan, Meera
Rastelli, Luca
Rieger, Daniel K.
Shenoy, Suresh G.
Shimkere, Richard A.
Spytek, Rimberly A.
Zhong, Mei
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Publication No. US20040259774A1
GENERAL INFORMATION:
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APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
APPLICANT: Gir, Xiaojia
APPLICANT: Ji, Weizhen
APPLICANT: Ji, Weizhen
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ORGANISM: Homo sapiens
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APPLICANT: Rastelli, Luca
APPLICANT: Rastelli, Luca
APPLICANT: Rieger, Daniel K.
APPLICANT: Shenoy, Suresh G.
APPLICANT: Sprek, Kimberly A.
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
CURRENT APPLICATION NUMBER: US/10/357,819
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                                                                                                                                                                                                          LPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQ 360
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NFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM
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Publication No. US20040259774A1
GENERAL INFORMATION:
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Miller, Charles E.
Padigaru, Muralidhara
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Rastelli, Luca
Rieger, Daniel K.
Shenoy, Suresh G.
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Ji, Weizhen
Kekuda, Ramesh
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                                                               121 IHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMA 180
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       503 MRGELWILVLVLVEBAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDR 562
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Publication No. US20040213793A1

GENERAL INFORMATION:
APPLICANT: Carson-Walter, Eleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELLAL CELL EXPRESSION PATTERNS
FILE REFERRINCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT PILLING DATE: 2003-10-14
PRIOR PLILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: PESSECE for Windows Version 4.0
SEQ ID NO 179
LENGTH: 1002
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Pred. No. 1.4e-248;
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US-10-474-794-179
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Best Local S
Matches 500
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Sequence 5, Application US/10156487A;
Publication No. US20030092025A1
GENERAL INFORMATION:
APPLICANT: Juan, Todd
APPLICANT: Juan, Todd
APPLICANT: Oliner, John
TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
FILE REFERENCE: 01-072-A
CURRENT APPLICATION NUMBER: US/10/156,487A
CURRENT APPLICATION NUMBER: 60/293,852
RIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 5.
LENGTH: 502
                                                                                                                                                                                                                                                                                                                      61 TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVK 120
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                                                                                                                                                                                                          Gaps
PRIOR APPLICATION NUMBER: 60/359,367
PRIOR FILING DATE: 2002-02-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 142
SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 4
LENGTH: 488
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                                                                                                                                                                         Score 2602; DB 17;
Pred. No. 1.7e-240;
1; Mismatches 0;
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Best Local Similarity 97.4%;
Matches 487; Conservative
                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
US-10-357-819-4
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ORGANISM: Homo sapiens
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                                                                                                                                               1 MRGELWLLVLVLREAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDR
                                                                                                   1 MRGELWLLVLVLREAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDR
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APPLICANT: Bert Vogelstein
APPLICANT: Bert Vogelstein
APPLICANT: Kenneth Kluzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REPREBNCB: 1107.00134
CURRENT APPLICATION UNMBER: 06/222,599
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
  Length
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Score 2566; DB 14;
Pred. No. 5e-237;
0; Mismatches 7;
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Best Local Similarity 81.6%; Pred. No. 9.6e-203;
Matches 409; Conservative 46; Mismatches 44;
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  Query Match
Best Local Similarity 95.9%;
Matches 487; Conservative
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Sequence 6, Application US/10156487A; Sequence 6, Application US/10156487A; Bedian No. US20030092025A1; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Union, Todd
APPLICANT: Oliner, John
TITLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
FILE REFERENCE: 01-072-A
CURRENT PILING DATE: 2002-09-10
PRIOR FILING DATE: 2002-09-10
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
IENGTH: 500
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                                       240 MSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFT 299
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                   KIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLM 179
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                                                                                     ANFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIP
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Best Local Similarity 81.6%; Pred. No. 9.6e-203;
Matches 409; Conservative 46; Mismatches 44;
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                                                                     KIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLM 179
                                                                                                                                          121 KIHRILSSSHRQASRVVLSFDFPFYGHPLRQITIATGGFIFWGDMLHRMLTATQYVAPLM 180
                                                                                                                                                                                          ANFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIP 239
                                                                                                                                                                                                                                                                          241 MAVLDISSAQHPVXAGLSBAFMILNSSPEVPESQRRTIFEYHRVELDSSKITTTSAVEFT 300
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                                                                                                                                                                                                                                                                                                                                 PLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDF 359
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MSVPE1SSSQHPVKTGLSDAFM1LNPSPDVPESRRRS1FEYHR1ELDPSKVTSMSAVEFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 297, Application US/09918715
; Bublication No. US20030017157A1
; GENERAL INFORMATION:
    APPLICANT: Brad St. Croix
; APPLICANT: Brad St. Croix
; APPLICANT: Brad St. Croix
; APPLICANT: Brad St. Croix
; APPLICANT: Brad St. Croix
; TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
; FILE REFERENCE: 1107.00134
; CURRENT APPLICATION NUMBER: US/09/918,715
; CURRENT APPLICATION NUMBER: 60/22,599
PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR APPLICATION NUMBER: 60/224,360
; PRIOR PILING DATE: 2000-08-11
; PRIOR PILING DATE: 2000-08-11
; PRIOR PILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0
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81.6%; Pred. No. 9.6e-203;
ive 46; Mismatches 44;
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; ORGANISM: Mouse
US-09-918-715-297
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US-09-918-715-297
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                                                                  420 TPVHLGTIVGIVLAVLLVAAIILAGIXINGHPTSNAALFFIERRPHWPAMKFRSHPDHS
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82.1%; Score 2209; DB 17;
Best Local Similarity 81.6%; Pred. No. 9.6e-203;
Matches 409; Conservative 46; Mismatches 44;
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APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Vogelaterin, Bert
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESS:
FILE REFERENCE: 1107.00179
FULR REPERENCE: 107.00179
CURRENT APPLICATION NUMBER: 60/282,850
PRIOR PILING DATE: 2003-10-14
PRIOR PILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
PRIOR FILING DATE: 2001-06-01
SPRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: PRESCE for Windows Version 4.0
SEQ ID NO 297
                                                                                                                                                                                                                                                     ; Sequence 297, Application US/10474794; Publication No. US20040213793A1; GENERAL INFORMATION:
                                                                                                                                                                    180 TYTEVEPSGHEKEGFVEAEQC 500
                                                                                                                                                    ; ORGANISM: Mouse US-10-474-794-297
                                                                                                                                                                                                                                       -10-474-794-297
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                                                    PLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAGRMCEDF 359
                                                                                                                   QDEDHDSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKG 419
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GENERAL INCOMMALON:
GENERAL INCOMMALON:
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Kinzler, Kenneth
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107 00179
CURRENT APPLICATION NUMBER: 06/282, 850
PRIOR APPLICATION NUMBER: 60/382, 850
PRIOR APPLICATION NUMBER: 60/308, 829
PRIOR FILING DATE: 2001-04-11
PRIOR APPLICATION NUMBER: 60/308, 829
PRIOR FILING DATE: 2001-06-11
PRIOR PILING DATE: 2001-06-11
SPRIOR FILING DATE: 2001-06-11
SPRIOR FILING DATE: 359
SOFTWARE: FABLESQ for Windows Version 4.0
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81.6%; Pred. No. 9.6e-203;
iive 46; Mismatches 44;
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                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 192, Application US/10474794; Publication No. US20040213793A1; GENERAL INFORMATION:
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ORGANISM: Mus musculus
US-10-474-794-192
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APPLICANT: Mize, Nancy APPLICANT: Marcy Nancy APPLICANT: Lee, Juhi
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: METHODS AND POLYNUCLEOTIDES
FILE REFERENCE: 30266/37630
CURRENT PAPLICATION NUMBER: US/10/168,365
CURRENT FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 36
LENGTH: 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 VVYFDNGTVFVVQWDHVYLQCWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHP 180
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Pred. No. 1.5e-200;
0; Mismatches 7;
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Job time : 138.657 secs
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Best Local Similarity 95.2%;
Matches 416; Conservative (
Chao, Cheng-Chi
Drmanac, Radoje T
Mize, Nancy
Lee, Juhi
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                                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-10-168-365-36
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TITLE OF INVENTION: METHODS AND MATRIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLECTIDES
TITLE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2010-07-24
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SOFTWARE: Patentin version 3.0
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81.2%; Score 2185; DB 10; Length 431;
Best Local Similarity 95.2%; Pred. No. 1.5e-200;
Matches 416; Conservative 0; Mismatches 7; Indels 14
                     TYAEVEPSGHEKEGFMEAEOC 500
                                         480 TYTEVEPSGHEKEGFVEAEOC 500
                                                                                                                                     US-09-912-935-36; Sequence 36, Application US/09912935; Publication No. US20030022825A1; GENERAL INFORMATION:
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APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Childs, John
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ORGANISM: Homo sapiens
US-09-912-935-36
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January 28, 2005, 21:52:02 ; Search time 158.818 Seconds (without alignments) 1129.372 Million cell updates/sec
GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-09-918-715-230 score: Perfect

1 MRGELWLLVLVLREAARALS......YAEVEPSGHEKEGFMEAEQC 500 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 88 Minimum | Maximum |

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2002s:\* geneseqp2003as:\* geneseqp2003bs:\* A\_Geneseq\_23Sep04:\* geneseqp1980s:\* geneseqp1990s:\* geneseqp2000s:\* geneseqp2001s:\* geneseqp2004s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

SUMMAKIES	ID Description	ABB90749 Abb90749 Human Tum	ABU54456 Human tum	ADI21063 Adi21063 Novel hum	ADH13230 Human mal		ADI21553 Novel hum	ABB90723 Human Tum	ABU54430 Abu54430 Human tum	ADI21064 Novel hum	ABB90783 Abb90783 Mouse Tur	ABB90729 Abb90729 Mouse Tum	ABU54436 Aouse tum	ABU54490 Mouse tum		ABO01434	AAB43131 Human ORF	AAB85396 Aab85396 Stem cell	ABO01430 Abo01430 Human ste	AAB85394 Stem cell	ABB90734 Abb90734 Human Tum		ABP53349 Human tra	ABG69157 Abg69157 Human ste	ABG69161 Human pro	
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	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	6.96	82.1	82.1	82.1	82.1	81.2	81.2	74.6	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	
	Score	2691	2691	2691	2691	2691	2691	2691	2691	2607	2209	2209	2209	2209	2185	2185	2007	1295	1295	1295	1295	1295	1295	1295	1295	
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## ALIGNMENTS

RESULT 1

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Human; mouse; rat; TEM; tumour endothelial marker; NEM; PEM; cytostatic; normal endothelial marker; immunostimulant; antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                           Human Tumour Endothelial Marker polypeptide SEQ ID NO 230.
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ABB90749 standard; protein; 500
                             (first entry)
                                                                                                                 WO200210217-A2.
                                                                                                    Homo sapiens
                             30-MAY-2002
                                                                                       psoriasis.
               ABB90749;
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07-FEB-2002

01-AUG-2001; 2001WO-US024031.

02-AUG-2000; 2000US-0225599P. 11-AUG-2000; 2000US-0224360P. 11-APR-2001; 2001US-0282850P.

(UYJO ) UNIV JOHNS HOPKINS.

B; Vogelstein St Croix B, Kinzler KW,

WPI; 2002-291856/33.

N-PSDB; ABL92103

An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.

Claim 1; Page 206-207; 331pp; English.

The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90740, ABB90749, ABB907569. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic

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retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL921996-ABL92041 and ABL92143-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
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                                                                                                                                                                100.0%; Score 2691; DB 5; Length 500; 100.0%; Pred. No. 3.1e-249;
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                                                                                                                                                                                        designated as tumor endothelial
                                                                                                                                                                                       New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      or
                                                                                                                                                                                                                                                                                                  The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tummour ECs. Tumour endothelial marker (TEM), normal endothelial marker (TEM), normal endothelial marker (TEM) genes are identified in human ECs. The human EC marker proteins and the polynucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are all useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducting an immune response to tumour endothelial cells in a patient, for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IHTILSNITHRQASRVVLSFDPPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFNPGYSDNSTVVYFDNGTVFVVQMDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRGELWLLVLVLVERAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDR
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                                                                                                             Kinzler KW, Vogelstein
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100.0%; Pred. No. 3.1e-249;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                       Disclosure; Page 221-222; 374pp; English.
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                                                                                                             Croix B,
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                            11-APR-2001; 2001US-0282850P.
06-FEB-2002; 2002US-0354262P.
10-APR-2002; 2002WO-US008253
                                                                             UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 500; Conservative
                                                                                                             Carson-Walter E, St
                                                                                                                                           WPI; 2003-093016/08.
N-PSDB; ABX72028.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 500 AA;
                                                                                                                                                                                                                                         psoriasis.
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IHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMA NPNPGYSDNSTVVYPDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM NFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM

IHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMA

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SVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTP

360

420 420

LPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQ 360

LPTCLOHRSCDACMSSDLTFNCSWCHVLORCSSGFDRYROEWMDYGCAQEAEGRMCEDFQ

DEDHDSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGT DEDHDSASPDISFSPYDGDLTTISSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGT PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAALFFIERRPHHWPAMKFRSHPDHST

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YAEVEPSGHEKEGFMEAEQC YAEVEPSGHEKEGFMEAEQC

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(first entry)

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241 SVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRKSIFEYHRIELDPSKVTSMSAVEFTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human malignant neoplasia-related protein SeqID79.
                                                                                                                                                                                                                                                                                                                                                                                                     ADH13230 standard; protein; 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide with biological activity. The polymorleotides and polypeptides are useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polymucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elloit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or respensation, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
                                                                                                                              forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; myence; and call disorder; lymphoid cell disorder; lissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue replacement; burn; incision; ulcer; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                   Wang J;
                                                                                                                                                                                                                                                                                                                                                                             Wang
                                                                                                                                                                                                                                                                                                                                                                RW, Ren F, Zhang J, Zhao QA,
Weng G, Zhou P, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 500;
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100.0%; Pred. No. 3.1e-249;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 20; SEQ ID NO 314; 156pp; English
                                  ADI21063 standard; protein; 500 AA
                                                                                                                                                                                                                                                                                                                                                                   Goodrich
Wehrman T,
                                                                                                                                                                                                                                                                                                       19-SEP-2001; 2001US-0323739P.
                                                                                                                                                                                                                                                                              19-SEP-2002; 2002WO-US029964
                                                                                   entry)
                                                                                                          Novel human protein #38.
                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                Tang YT, Asundi V,
Ghosh M, Xue AJ, W
Haley-Vicente D;
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N-PSDB; ADI21779.
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500; Conserv
                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC
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                                                                                                                                                                                                        Homo sapiens.
                                                                                  15-APR-2004
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replacement
                                                                                                                                                                                                                                                       27-MAR-2003
                                                          ADI21063
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           RESULT 3
                        ADI21063
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Predicting, diagnosing or prognosing malignant neoplasia by detecting at least two markers, where the markers are genes from one or more chromosomal regions altered in malignant neoplasia,.
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                         gastric cancer; colon cancer; oesophageal cancer; mesenchymal cancer;
bladder cancer; non-small cell lung cancer; human.
malignant neoplasia; cytostatic; breast cancer; ovarian cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; SEQ ID NO 79; 267pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kallabis H;
                                                                                                                                                                                                                                                                                                                                                       09-MAY-2003; 2003EP-00010447.
                                                                                                                                                                                                                                                                                                                                                                                                                          21-MAY-2002; 2002EP-00010291
13-FEB-2003; 2003EP-00003112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Munnes M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-073279/08.
N-PSDB; ADH13207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FARB ) BAYER AG
                                                                                                                                            Homo sapiens
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Gaps

Indels

Conservative

Local Best Loca Matches 9

61 TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVK 120

1 MRGELWLLVLVLREAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDR

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Wang

Zhao QA,

19-SEP-2001; 2001US-0323739P. 19-SEP-2002; 2002WO-US029964

WO2003025148-A2 Homo Bapiens

27-MAR-2003

(HYSE-) HYSEQ INC

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cytostatic compounds through the regulation of the expression of a gene or activity of a protein associated with malignant neoplasia. The method is useful for prediction, diagnosis or prognosis of malignant neoplasia such as breast cancer, ovarian cancer, gastric cancer, colon cancer, oesophageal cancer, wesenchymal cancer, pladder cancer or non-small cell lung cancer. The polymucleotides and polypeptides defined in the specification, antisense polymucleotides targeting the polymucleotides and compounds identified by the screening methods are useful for preventing or treating malignant neoplasia. The disease treated is preferably breast cancer. The present sequence is that of a human malignant neoplasia. The disease di numan malignant neoplasia.
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                                                                                                                                                                                                                                                                                                   100.0%; Score 2691; DB 8; Length 500; 100.0%; Pred. No. 3.1e-249;
                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                             pred. No. 3.1e-249;
0; Mismatches 0;
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Matches 500; Conservative
                                                                                                                                                                                                                                                               Sequence 500 AA;
                                                                                                                                                                                                                             the invention.
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The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in dagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating mythoid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or egeneration, in wound healing in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 IHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATGYVAPLMA
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ou P, Drmanac RT,
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100.0%; Pred. No. 3.3e-249;
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Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P,
Haley-Vicente D;
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SNINGO UNIV JOHNS HOPKINS
Sequence 527 AA;
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11-AUG-2000;
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                      PVHLGTIVGIVLAVLLVAAIILAGIYINGHPTSNAALFFIERRPHHWPAMKFRSHPDHST 480
                                                                                                      forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; hymphoid cell disorder; bone cartilage tissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue replacement; burn; incision; ulcer; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
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Weng G, Zhou P, Drmanac RT, Wang D;
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Wehrman T,
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13-SEP-2002; 2002US-00323739.
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N-PSDB; ADI21333.
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Haley-Vicente D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 NFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM
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                                                                                                                                                                                                           TOLSODLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVK
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100.0%; Score 2691; DB 7;
100.0%; Pred. No. 3.3e-249;
ive 0; Mismatches 0;
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                                                                                                                    The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a ABB90749, ABB90713, ABB90730, ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, necanglogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and refine are disclosed, as are marker oligonucleotide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92141-ABL92191; normal endothelial markers (NEM) ABL92042-ABL92041 and ABL92191-10 inormal (PEM) ABL91903-ABL91995
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           Vogelstein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New purified human transmembrane protein, designated as tumor endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a novel method for the isolation of endothelial cells (ECs), and the identification of genes expressed in normal and tumour ECs. Tumour endothelial marker (TEM), normal endothelial marker (FEM), normal endothelial marker (FEM), normal polymucleotide sequences encoding them are useful for detecting, diagnosing or treating tumours as well as polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis, and psoriasis. They are also useful for inhibiting neoangiogenesis or tumour angiogenesis, for inducing an immune response to tumour andiogenesis, for for identifying candidate drugs for treating tumours. The present sequence represents a human TEM or NEM protein of the invention
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                                                                                                                                                                            pan-endothelial marker; polycystic kidney dieease; psorlasis; diabetic retinopathy; rheumatoid arthritis; tumour angiogenesis; neoangiogenesis; immune response; cytostatic; antidiabetic; ophthalmological; antirheumatic; antiarthritic; antipsoriatic.
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                                                                                                                                                        endothelial marker; normal endothelial marker; PEM;
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                                                                                                                         tumour endothelial cell;
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                                                            Human tumour endothelial marker TEM 8.
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Matches 500; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotides and secreted proteins, useful for treating myeloid or phoid cell disorders, in bone cartilage, tendon, ligament and nerve sue growth or regeneration, in wound healing, and in tissue repair and
                                                                                                                                                                                                                                                                                                                                                           forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; bone cartilage tissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing tissue repair; tissue replacement; burn; incision; ulcer; cancer; human.
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Wang D;
LPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQ
                                                     DEDHDSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGT
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Drmanac RT,
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3 G, Zhou P,
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shrman T, Weng G,
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2002US-00323739.
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Ghosh M, Xue AJ, W
Haley-Vicente D;
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N-PSDB; ADI21780.
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13-SEP-2002;
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normal endothelial marker; pan-endothelial marker; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiangiogenic; tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease; diabetes; retinopathy; rheumatoid arthritis;
                                                                                                                                                                                                                                             1 MRGELWLLVLVLREAARALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDR
                                                                                                                                                                                                                                                                                                           121 IHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMA
                                                                                                                                                                                                                                                                                                                                                                               IHTILSNTHROASRVVLSFDFPFYGHPLROITIATGGFIFMGDVIHRMLTATQYVAPLMA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NFNPGYSDNSTVVYFDNGTVFVVQMDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVPEISSSQHPVKTGLSDAFMILNPSPDVPBSRRRSIFEYHRIELDPSKVTSMSAVEFTP
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diseased tissues, for treating myeloid or lymphoid cell disorders, in
                                                                                                                                                                                      Gaps
              bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
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                                                                                                                                                   Score 2607; DB 7;
Pred. No. 3.5e-241;
0; Mismatches 0;
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                                                                                                                                               96.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; protein;
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                                                                                                                                                                     Similarity 97.6
88; Conservative
                                                                                                                     Sequence 488 AA;
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                                                                                                                                                   Query Match
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Sequence 500 AA;
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                                                                                                                                                                                                     psoriasis.
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ID ABB9
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                                                                                                                                                                                                                                  variable region which specifically binds to an extracellular domain of a tumour endothelial marker (TEM) protein selected from ABB90732, ABB90749, ABB90749, ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABL92075-ABL92141 and ABB90721-ABB90789) are disclosed, as are marker oligonuclectide sequences: tumour endothelial markers (TEM) ABL91996-ABL92041 and ABL92193-ABB92191; normal endothelial markers (TEM) ABL92042-ABL92074; and pan-endothelial markers (PEM) ABL91995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                  An isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a tumor endothelial marker (TEM) protein, useful for inhibiting tumor growth.
                                                                                                                                                                                                                             The invention relates to an isolated molecule comprising an antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                82.1%; Score 2209; DB 5; Length 5
81.6%; Pred. No. 6.7e-203;
.ive 46; Mismatches 44; Indels
                                                                                                                                                                                                  Disclosure; Page 301-302; 331pp; English.
                                                                                     Vogelstein
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          02-AUG-2000; 2000US-0225599P.
11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
                                                            (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                           al Similarity 81.6
409; Conservative
                                                                                      Kinzler KW,
                                                                                                              2002-291856/33.
                                                                                                                          N-PSDB; ABL92136
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 500 AA;
                                                                                     Croix B,
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The invention relates to an isolated molecule comprising an antibody variable region which specifically binds to an extracellular domain of a ABB90749, ABB90750 and ABB90769. The antibodies which bind to TEM proteins have cytostatic, immunostimulant and antiangiogenic activity. They are useful for inhibiting tumour growth, neoangiogenesis in subjects bearing a vascularised tumour, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis and psoriasis. Human, mouse and rat TEM genes and the encoded proteins (ABB20775-ABB91141 and ABB90771-ABB90789) are disclosed, as are marker oligonucleotide sequences: tumour endochelial markers (TEM) ABL92041-ABL92191, normal endothelial markers (NEM) ABL92042-ABL92074; and pan-endothelial markers
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                                                                                                                                                                                                                                                                               Human, mouse, rat, TEM, tumour endothelial marker, NEM, PEM, cytostatic, normal endothelial marker; jamunostimulant, antiangiogenic, tumour; neoangiogenesis; vascularised tumour; polycystic kidney disease, diabetes; retinopathy; rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 KIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLM
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                                                                                                                                                                                                               Mouse Tumour Endothelial Marker polypeptide SEQ ID NO 192.
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ABB90729 standard; protein; 500
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11-AUG-2000; 2000US-0224360P.
11-APR-2001; 2001US-0282850P.
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The present invention relates to a novel method for the isolation of endothelial cells (BCs), and the identification of genes expressed in normal and tumour BCs. Tumour endothelial marker (FEM), normal endothelial marker (NEM), and pan-endothelial marker (PEM) genes are identified in human BCs. The human BC marker proteins and the

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                                                                                                                                                                                                                                                     New purified human transmembrane protein, designated as tumor endothelial marker (TEM) 3, useful for detecting, diagnosing or treating tumors, polycystic kidney disease, diabetic retinopathy, rheumatoid arthritis or psoriasis.
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                                                                                                                                                                 Vogelstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 2209; DB 6;
; Pred. No. 6.7e-203.
46; Mismatches 44.
                                                                                                                                                                 Kinzler KW,
                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 339-340; 374pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500
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                                                                                                                                                               St Croix B,
                                           11-APR-2001; 2001US-0282850P
06-FEB-2002; 2002US-0354262P
.0-APR-2002; 2002WO-US008253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity 81.6%;
409; Conservative 4
                                                                                                                 SNING OLYU) (OLYU)
                                                                                                                                                                                                            WPI; 2003-093016/08.
                                                                                                                                                            Carson-Walter E,
                                                                                                                                                                                                                                     N-PSDB; ABX72061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 500 AA;
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Best Local 9
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The invention provides novel human stem cell growth factor-like polypeptides and polymclocides encoding them. The polypeptides having stem cell growth factor-like activity, can be expressed by standard recombinant methodology. The polymcleotides and polypeptides can be used to induce differentiation of embryonic and adult stem cells to give rise to different cell types. They may also be used in the treatment of leukemia, hemophilia, and degenerative diseases like Alzhaimer's disease. They may also be utilized to generate new tissues and organs that may aid supplements in need of transplants. They can also be used as nutritional supplements. The present sequence represents a tumour endothalial marker in precein, homologous to a stem cell growth factor-like
                                                                                                                                                                                                               Stem cell growth factor-like polypeptide; leukemia; hemophilia; human; degenerative disease; Alzheimer's disease; untritional supplement; cytostatic; nootropic; neuroprotective; hemostatic; antisense-therapy; gene-therapy; tumour endothelial marker 7 precursor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVYPDNGTVEVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     132 ASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Childs J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated polypeptide with stem cell growth factor-like activity for treatment of leukemia, hemophilia, and degenerative diseases like Alzheimer's disease and to generate new tissues and organs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mize NK,
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Pred. No. 1.1e-200;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee J,
                                                                                                                                                                                 Tumour endothelial marker 7 precursor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 149-150; 154pp; English.
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TYTEVEPSGHEKEGFVEAEQC 500
                                                                                 protein; 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JAN-2000; 2000US-00488725.
07-APR-2000; 2000US-00545714.
11-APR-2000; 2000US-00547358.
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95.2%;
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                                                                                 AAB85400 standard;
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                                                                                                                                                                                                                                                                                                                                    WO200153500-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1999;
                                                                                                                                                  17-SEP-2001
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                                                RESULT 14
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VKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCD 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New stem cell growth factor-like polypeptides and polymucleotides, useful for treating e.g. leukemia, hemophilia, osteoporosis, osteoarthritis, graft-versus-host disease, cancers, Alzheimer's disease, Huntington's
VVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHP 180
                                                                                                                                                                ACMSSDLTFNCSWCHVLQRCSSGFDRYRQEW-MDYGCAQEAEGRMCEDFQD-----ED 363
                                                                                                                                                                                                                      294
                                                                                                                                                                                                                                                                                                              TTSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGGGLQNNLSPKTKGTPVH 354
                                                                                                                                                                                                                                                                                                                                                                                      LGTIVGIVLAVLLVAAIILAGIYINGHPTSNAALFFIERRPHHWPAMKFRSHPDHSTYAE 483
                                                                                                                                                                                                                                                                                                                                                                                                                   VKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCD
                                                                                                                                                                                                                                                                         HDSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endothelial marker 7 precursor protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB001434 standard; protein; 431 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEPSGHEKEGFMEAEQC 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEPSGHEKEGFMEAEQC 431
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DRMANAC R T.
TANG Y T.
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(TANG/)
(CHAO/)
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The invention relates to a new isolated polypeptide, which has stem cell growth factor-like activity. The new polypeptide, the polymucleotide encoding this polypeptide, or the agonist of the polypeptide are useful for treating a subject in need of enhanced activity or expression of stem cell growth factor-like polypeptide. The antagonist of the polypeptide or

Example 4; Fig 2; 98pp; English.

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the polynucleotide is useful for treating a subject in need to indicate the activity or expression of stem cell growth factor-like polypeptide. The new polypeptide or polynucleotide is particularly useful for inducing differentiation of embryonic and adult stem cells to give rise to different cell types. In particular, the polypeptide or polynucleotide is useful for treating leukaemia, haemophilia, osteoporosis, osteoparthritis, canaemia, tendonitis, carpal tunnel syndrome, autoimmune diseases (e.g. multiple sclerosis, systemic lupus erythematosus, graft-versus-host cisease or allergies), cancers or degenerative disease (e.g. Alzheimer's cisease, parkinnon's disease, huntington's disease (e.g. Alzheimer's clisease or allergies), thutington's disease or amyotrophic lateral collisease or canyotrophic lateral collisease or the treatment of these diseases. The new polypeptide or collinearing new tissues and organs that may aid patients in need of transplanted tissues. The polynucleotide may also be used in comparation of these diseases. The new polypeptide or plynucleotide is also useful in diagnostic or research methods. The correspondent sequence represents the human tumour endothelial marker 7
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1 YHRIELDPSKVTSMSAVEFT.......CHVLQRCSSGFDRYRQEWMD 65
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1. cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2. cgn2 6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

3. cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	tion	nce 4, Appli	Sequence 230, App	nce 79, Appl	nce 230, App			nce 179, App		nce 36, Appl	5, 7		nce 297, App	nce 6, Appli
	Description	Segue	Sedne	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	αı	US-10-357-819-4	US-09-918-715-230	US-10-435-696-79	US-10-474-794-230	US-10-357-819-2	US-09-918-715-179	US-10-474-794-179	US-09-912-935-36	US-10-168-365-36	US-10-156-487A-5	US-09-918-715-192	US-09-918-715-297	US-10-156-487A-6
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193	Sequence 12, Appl.1 Sequence 12, Appl Sequence 193, App Sequence 299, App Sequence 2, Appl.1 Sequence 23, Appl.1	25,000	w w w w u u u v	Sequence 40, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 472, Apples Sequence 4
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## ALIGNMENTS

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APPLICANT: Spytek, Kimberly A.
APPLICANT: Zhong, Mei
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/357,819
CURRENT FILING DATE: 2003-02-03
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PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/783,436
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2002-02-25
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: 60/353,301
             Sequence 4, Application US/10357819
Publication No. US20040259774A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           Patturajan, Meera
Rastelli, Luca
Rieger, Daniel K.
Shenoy, Suresh G.
Shimkets, Richard A.
Spytek, Kimberly A.
                                                                                                                                                                                                                                                                                                      Padigaru, Muralidhara
                                                                                                   Edinger, Shlomit R. Gangolli, Esha A. Gerlach, Valerie L. Gorman, Linda Guo, Xiaojia Ji, Weizhen Kekuda, Ramesh
                                                                                                                                                                                                                                                                                Charles E
                                                                                 APPLICANT: Alvarez, Enrique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 21402-538A
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Miller,
JS-10-357-819-4
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APPLICANT:
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PRIOR FILING DATE: 2002-02-01

PRIOR PLING DATE: 2002-02-08

PRIOR FILING DATE: 2002-02-08

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PRIOR PLICATION NUMBER: 60/356,424

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Sequence 230, Application US/09918715

Publication No. US20030017157A1

GENERAL INFORMATION:

APPLICANT: Berd &L. Croix

APPLICANT: Berd &L. Croix

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134

CURRENT FILING DATE: 2001-08-01

PRIOR PELICATION NUMBER: 60/224,599

PRIOR PELICATION NUMBER: 60/224,599

PRIOR PELICATION NUMBER: 60/224,360

PRIOR PELICATION NUMBER: 60/224,360

PRIOR PILING DATE: 2000-08-01

PRIOR PILING DATE: 2000-08-01

NUMBER: OF SEQ 1D NOS: 358

SOFTWARE: FEST ENDOTHELIAL

LENGTHELS OF SEQ 1D NOS: 358

LENGTHELS OF SEQ 1D NOS: 358

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Best Local Similarity 100.0%; Pred. No. 1.8e-36;
Matches 65; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 370; DB 10;
100.0%; Pred. No. 1.9e-36;
tive 0; Mismatches 0;
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Best Local Similarity 100.
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; ORGANISM: Homo sapiens
US-09-918-715-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , ORGANISM: Homo sapiens
US-10-357-819-4
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RESULT 3

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Sequence 79, Application US/10435696

Sequence 79, Application US/10435696

Sequence 79, Application US/10435696

Sequence 79, Application No. US20040018525A1

GENERAL INFORMATION:

APPLICANT: Witter, Rallabis, Harald

APPLICANT: Kallabis, Harald

TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA

TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA

TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA

TITLE OF INVENTION: PREVENTION AND TREATMENT OF MALIGNANT NEOPLASIA

FILE REPERENCE: Lepo3003112.4

PRIOR APPLICATION NUMBER: EP02010291.9

PRIOR FILING DATE: 2002-05-21

NUMBER OF SCO ID NOS: 314

SCOTUMARE: PatentIn version 3.1

SEQ ID NO 79

FURNIAL SOO
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APPLICANT: Carcoix, Brad
APPLICANT: Carcoix, Brad
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: PSESSEQ for Windows Version 4.0
SEQ ID NO 230
LENGTH: 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 370; DB 15; Best Local Similarity 100.0%; Pred. No. 1.9e-36; Matches 65; Conservative 0; Mismatches 0;
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o. US20040213793A1
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US-10-474-794-230
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US-10-435-696-79
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Best Local Similarity 100.0%; Pred. No. 3.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0;
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                                                                          APPLICANT: Braf St. Croix
APPLICANT: Braf St. Croix
APPLICANT: Braf St. Croix
APPLICANT: Braf St. Croix
TITLE OF INVENTION: ENDORMELLAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-01
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
STORY FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
STORY FILING DATE: 2000-08-11
STORY FILING DATE: 2000-08-11
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Carcion.Walter, Eleanor

APPLICANT: Carcion.Walter, Eleanor

APPLICANT: St. Croix, Brad

APPLICANT: Vogelstein, Bert

APPLICANT: Windler, Kenneth

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REPERENCE: 1107.00179

CURRENT APPLICATION NUMBER: US/10/474,794

CURRENT FILING DATE: 2001-04-11

PRIOR APPLICATION NUMBER: 60/282,850

PRIOR PLILING DATE: 2001-04-11

FRIOR PLILING DATE: 2001-04-11

FRIOR PLILING DATE: 2001-04-11

SROR PRILING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 359

SOFTWARE: FastsEQ for Windows Version 4.0
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Sequence 179, Application US/09918715
Publication No. US20030017157A1
GENERAL INFORMATION:
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Publication No. US20040213793A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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CRGANISM: Homo sapiens
US-10-474-794-179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 YHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYR 339
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NUMBER OF SEQ ID NOS: 142
SOFTWARE: CuraSeqList version 0.1
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100.0%; Score 370; DB 17; Length 500;
Best Local Similarity 100.0%; Pred. No. 1.9e-36;
Matches 65; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE KEEKEKECE: 12402-5348

CURRENT PELLING DATE: 2003-02-03

PRIOR FULING DATE: 2003-02-03

PRIOR FILING DATE: 2003-02-03

PRIOR FILING DATE: 2000-05-31

PRIOR FILING DATE: 2000-05-31

PRIOR FILING DATE: 2000-05-31

PRIOR FILING DATE: 2001-02-14

PRIOR FILING DATE: 2001-02-14

PRIOR FILING DATE: 2001-02-14

PRIOR APPLICATION NUMBER: 09/783,436

PRIOR FILING DATE: 2002-02-25

PRIOR PILING DATE: 2002-02-01

PRIOR PILING DATE: 2002-02-01

PRIOR PILING DATE: 2002-02-09

PRIOR PELING DATE: 2002-02-09

PRIOR PELING DATE: 2002-02-09

PRIOR PILING DATE: 2002-02-0

PRIOR PILING DATE: 2002-02-0

PRIOR PILING DATE: 2002-02-0

PRIOR PILING DATE: 2002-02-0

PRIOR PILING DATE: 2002-02-0

PRIOR PILING DATE: 2002-02-0

PRIOR PILING DATE: 2002-02-0

PRIOR PILING DATE: 2002-02-0

PRIOR PILING DATE: 2002-02-0

PRIOR PILING DATE: 2002-02-01

PRIOR PILING DATE: 2002-02-01
                                                                                                              Sequence 2, Application US/10357819
Publication No. US20040259774A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Li, Li
Miller, Charles B.
Padigaru, Muralidhara
                                                                                                                                                                                           APPLICANT: Alvarez, Enrique
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
APPLICANT: Guo, Xiaojia
APPLICANT: Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rastelli, Luca
Rieger, Daniel K.
Shenoy, Suresh G.
Shimkets, Richard A.
Spytek, Kimberly A.
Zhong, Mei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patturajan, Meera
                                                                                                                                                                                                                                                                                                                                                                                                      Kekuda, Ramesh
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ORGANISM: Homo sapiens
US-10-357-819-2
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QEWMD 344
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LENGTH: 500
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842 QEWMD 846

US-09-918-715-179

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280 YHRIELDPSKVTSMSAVEPTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYR 339
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                                                                                      APPLICANT: Juan, Todd
APPLICANT: Bass, Michael B.
APPLICANT: Bass, Michael B.
APPLICANT: Diner, John
TITLE OF INVENTION: Tunc Endothelial Marker 7a Molecules and Uses Thereof
FILE REFERENCE: 01-072-A
CURRENT APPLICATION NUMBER: US/10/156,487A
CURRENT FILING DATE: 2002-09-10
PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 YHRIBLDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYR 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 192, Application US/09918715

Publication No. US20030017157A1

GENERAL INFORMATION:

APPLICANT: Brad St. Croix

APPLICANT: Bert Vogelstein

APPLICANT: Bert Wogelstein

TITLE OF INVENTION: BNDOTHELIAL CELL EXPRESSION PATTERNS

TITLE PET INVENTION: 101074

CURRENT PILION DATE: 2001-08-01

PRIOR APPLICATION NUMBER: 60/22,599

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR APPLICATION NUMBER: 60/224,360

PRIOR PILING DATE: 2000-08-02

PRIOR FILING DATE: 2000-08-11

PRIOR FILING DATE: 2000-04-11

NUMBER OF SEQ ID NOS: 358

SOFTWARE: FESTER OF Windows Version 3.0

LENGTH: 500
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97.0%; Score 359, DB 14;
Best Local Similarity 100.0%; Pred. No. 4.1e-35;
Matches 63; Conservative 0; Mismatches 0;
                 Sequence 5, Application US/10156487A publication No. US20030092025A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 502
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ORGANISM: Mus musculus
US-09-918-715-192
                                                                                                                                                                                                                                                                                                                                                                                                                            CRGANISM: Homo sapiens US-10-156-487A-5
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APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Liu, Chenghua
APPLICANT: Liu, Chenghua
APPLICANT: Chao, Cheng-Chi
APPLICANT: Drmanac, Radoje T
APPLICANT: Dres, Uni
APPLICANT: Lee, Juhi
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
FILE REPERENCE: 30266/37630
CURRENT APPLICATION NUMBER: US/10/168,365
CURRENT FILING DATE: 2000-12-22
SURNER PETEL OF DNOS: 36
SOFTWARE: Patentin version 3.0
                                                                                    APPLICANT: Nishikawa, Mitsuo et al.

TITLE OF INVENTION: METHODS AND MATRIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REPERBNCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT PILING DATE: 2001-07-24
PRIOR PILING DATE: 2000-10-724
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 36
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                 Sequence 36, Application US/09912935
Publication No. US20030022825A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-10-168-365-36
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JS-09-912-935-36
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LENGTH: 431
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281 YHRVELDSSKITTTSAVEFTPLPTCLQHQSCDTCVSSNLTFNCSWCHVLQRCSSGFDRYR 340
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Pred. No. 5.7e-31;
                                                                                                GENOUAL 4-4-794-192

| Sequence 192, Application US/10474794
| Publication No. US20040213793A1
| GENERAL INFORMATION:
| APPLICANT: Carson-Walter, Eleanor
| APPLICANT: Carson-Walter, Eleanor
| APPLICANT: St. Croix, Brad
| APPLICANT: Kinzler, Kenneth
| TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
| TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
| FILE REPRENCE: 1107.00179
| CURRENT FILING DATE: 2003-10-14
| PRIOR PILING DATE: 2001-04-11
| PRIOR PILING DATE: 2001-04-01
| NUMBER OF SEQ ID NOS: 359
| SOFTWARE: FastSEQ for Windows Version 4.0
| SEQ ID NO 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Mismatches
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Best Local Similarity 84.4%;
Matches 54; Conservative
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Best Local Similarity 84.44
Matches 54; Conservative
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                      341 QEWL 344
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Publication No. US20
GENERAL INFORMATION:
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; Bedrard. INFORMATION:
    APPLICANT: Uses, Michael B.
    FILE REFERENCE: 01-072-A
    CURRENT FPLING DATE: 2002-09-10
    PRIOR PILING DATE: 2002-09-10
    NUMBER OF SEQ ID NOS: 15
    SOFTWARE: Patentin Ver. 2.0
    SEQ ID NO 6.
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84.4%; Pred. No. 5.7e-31;
tive 7; Mismatches 3; Indels (
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84.4%; Pred. No. 5.7e-31;
ive 7; Mismatches 3; Indels (
                                                                                                     Sequence 297, Application US/09910715;
Sequence 297, Application No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad &C. Croix
APPLICANT: Bert Vogelstein
APPLICANT: Reneeth Kinzler
TILE OF INVENTION: RNOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT PILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR PILING DATE: 2000-08-02
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 2000-08-11
PRIOR PLING DATE: 3000-08-11
PRIOR PLING DATE: 3000-08-11
SPRIOR PLING DATE: 3000-04-11
SPRIOR PLING DATE: 3000-04-11
SQUING PLING DATE: 3000-04-11
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 84.4
Matches 54; Conservative
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Matches 54; Conservative
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341 QEWL 344
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US-09-918-715-297
                                                                                             US-09-918-715-297
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Pred. No. 5.7e-31;
7; Mismatches 3; Indels
APPLICANT: Cargon-Walter, Bleanor
APPLICANT: Cargon-Walter, Bleanor
APPLICANT: Cargon-Walter, Brad
APPLICANT: Vogelstein, Bart
APPLICANT: Vogelstein, Bert
APPLICANT: Winglerer, Kenneth
TITHE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107 00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT PILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/382,850
PRIOR FILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-04-11
SROFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 500
TYPE: PRI
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61 QEWM 64 |||: 341 QEWL 344

Search completed: January 28, 2005, 22:19:19 Job time: 18.7655 secs

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January 28, 2005, 21:55:58 ; Search time 28.3934 Seconds (without alignments) 1389.370 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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2218
                                                                                                 OM protein - protein search, using sw model
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1 ALSPQPGAGHDEGPGSGWAA......GLQNNLSPKTKGTPVHLGTI 410 283416 283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Scoring table: Sequence: Searched:

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

PIR 79:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote alpha tectorin - c NEDD-4 ORF - mouse neprilysin (EC 3.4 ubiquitin ligase N protein-tyrosine-p PTP 35 protein - m sodium channel alp phosphoenolpyruvat IFH1 protein - yea IFH1 protein - yea hypothetical prote hypothetical prote 2a protein - broad mucin 5AC (clone L pregnancy specific phosphoenolpyruvat phosphoenolpyruvat hypothetical prote hypothetical prote probable membrane corticosteroid-bin hypothetical prote nidogen precursor semaphorin recepto EH domain protein ypothetical prote phosphoenolpyruvat probable cellulose protein tyrosine Description SUMMARIES AG3506 S55352 P2WMBB A57534 JN0067 I58345 T05673 Query Match Length DB 91.5 91.5 91.5 90.5 90 90 90 115.5 101.5 100.5 99 Result No. 

pregnancy-specific	sodium channel pro	hypothetical prote	hypothetical prote	hypothetical prote	alpha tectorin - m	pectate lyase (EC	related to DRPLA p	protein-tyrosine-p	ALR protein - huma	ALR protein - huma	Rag-2 protein - ch	semaphorin homolog	dynein heavy chain	killer toxin insen	ZK112.7 protein -
A34595	CHRTM1	T31610	T15063	A84133	T30197	JC7653	T49849	S51005	T03455	T03454	842510	T03102	T30880	S51471	S44887
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424	1840	673	934	946	2155	441	538	1175	4957	5262	528	653	1123	1349	3343
4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0	4.0
89.5	89.5	8	83	89	89	88.5	88.5	88.5	88.5	88.5	88	88	88	88	88
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

CESP: C3

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Wed Feb

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                                                                                                                                                                                                                                                              A; Residues: 1-1161 < RNA
A; Residues: 1-1161 < RNA
A; Residues: 1-1161 < RNA
A; Residues: 1-1161 < RNA
A; Coserve = references: UNIPROT: Q04901; EMBL: D14018; NID: g217363; PIDN: BAA03127.1; PID: g2173
C; Superfamily: Ascidian nidogen; EGF homology; LDL receptor YWTD-containing repeat homol
C; Keywords: basement membrane; collagen binding; disulfide bond; duplication; extracellu
C; Keywords: basement membrane; collagen binding; disulfide bond; duplication; extracellu
C; Keywords: basement membrane; collagen binding; disulfide bond; duplication; extracellu
C; Keywords: basement membrane; greatus predicted < MAT>
F; L-106 / Domain: EGF homology < G1>
F; L-106 / Domain: BGF homology < G1>
F; S274-306 / Domain: thyroglobulin type I repeat homology < THY2>
F; 680-748 / Domain: LDL receptor YWTD-containing repeat homology < YW3>
F; 980-1013 / Domain: LDL receptor YWTD-containing repeat homology < W4>
F; 1032-1075 / Domain: LDL receptor YWTD-containing repeat homology < YW5>
F; 1129-1158 / Domain: EGF homology < EG2>
F; 1129-1158 / Domain: EGF homology < EG3>
F; 1129-1158 / Domain: EGF homology < EG3>
F; 107,334,360,484 / Binding site: carbohydrate (ABN) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
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C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T09074
R;Comeau, M.R.; Johnson, R.; DuBose, R.F.; Petersen, M.; Gearing, P.; van den Bos, T.;
Immunity 8, 473-482, 1998
A;Title: A poxyrius-encoded semaphorin induces cytokine production from monocytes and b
A;Reference number: Z16555; MUID:98246049; PMID:9586637
A;Accession: T09074
A;Accession: T09074
A;Accession: T09074
A;Residues: 1-1568 <COM>
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nidogen precursor - sea squirt (Halocynthia roretzi)
NyAlternate names: entactin
C;Species: Halocynthia roretzi
C;Date: 30-Sep-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C;Accession: S31213
R;Nakae, H.; Sugano, M.; Ishimori, Y.; Endo, T.; Obinata, T.
Blur, J. Blochem. 213, 11-19, 1993
A;Title: Ascidian entactin/nidogen. Implication of evolution by shuffling two kinds of A;Reference number: S31213; MUID:93238676; PMID:8477687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --FNPGYSDNSTVVY------FDNGTVFVVQWDHVYLQGWEDKGSFTFQAA 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LHHDGRIVFA---YKEIPMSVPEIS----SSQHPVKTGLSDA----FMILNPSP----DV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQ 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----HVKK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIFFREHKONATIARANTDVREAFIETAGDFNAGSVFVVTWDKVQSASREDGVTFTFQCI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 LSFDFPFYGHPLRQITIATGGFIFM-----GDVIHRMLTATQYVAPLMAN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
5.7%; Score 126; DB 1; Length 1161;
Best Local Similarity 23.5%; Pred. No. 0.059;
Matches 64; Conservative 34; Mismatches 88; Indels 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 AGSQGQWIFQIGGIMFNNDEASKESE-----KH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 RCSSGFDRYRQEW-MDYGCAQEAE-GRMCEDF 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 TROSGFOVSEVNFNEDFNIDLEAECGTPCSDF 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165
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A,Cross-references: UNIPROT:060486; EMBL:AF030339; NID:g3176761; PIDN:AAC18823.1; PID:g3
A,Experimental source: tissue type foreskin; cell type fibroblast
C,Genetics:
A,Gene: VSSPR
C,Keywords: receptor; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-743 xYRM-
A;Residues: 1-743 xYRM-
A;Cross-references: UNIPROT:054916; EMBL:AF031939; NID:92677842; PIDN:AAB94736.1; PID:92
A;Experimental source: cell line: C2C12; tissue type: muscle
                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 DVAE------ANRSQVKIHTILS-NTHRQASRVVLSFDFPFYGHPLRQITIAT 138
                                                                                                                                                                                                                                                                                                                                                                                              293 LILSSSLVEALDVWAGVFSAAAGEGGERRSPTTTALCLFRMSEIQARAKRVSWDFKTAES 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRI--VFAYKEIPMSVPEI---SSSQ 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 CDACMSSDLTFNCSWCHVLQRCSSGFDRYRQE----WMDYGCAQEAEGRMCEDFQ----D 344
                                                                                                                                                                                                                                                                                                                                                                 78 RLYGPSEPHSRELWVDV--AEANRSQVKIHTI-----LISNTHRQASRVVLSF---- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----DFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVY 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 HPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRS 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   423 TPV-----FYKLVPDP-----VKNIYIY------LTAGKEVRRIRVANCNKHKS 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 HCKEGDOPERVOPIASSTL------IHSDLTSV-YGTVVM------NRTVLF 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39 SEPDRIQLSQ-----DLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWV
                                                                                                                                                                                                                                                                GTVRGWNRRARESPGHVSEPDRT----QLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                              Indels 137;
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                                                                                                                                                                                                                                                                                                             256 GAATGWPSMAR----IAQSTEVLFQGQASLDCGHGH-----PDGR----
                                                                                                                                                             Length 1568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 743;
                                                                                                                                                          Query Match 5.2%; Score 115.5; DB 2; Best Local Similarity 20.6%; Pred. No. 0.67; Matches 77; Conservative 42; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.6%; Score 101.5; DB 2;
Best Local Similarity 18.3%; Pred. No. 3.5;
Matches 91; Conservative 63; Mismatches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 SERPLIGPGPFWSPFGDAQAGSSAGDAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 LSPOPGAGH-DEGPGSGWAAK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEKTTVTMVGSFSP 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           345 EDHDSASPDTSFSP 358
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C,Keywords: signal transduction
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Wed Feb

180		OY 196 WEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSGHPVKTGLSDAFMIL 246       :   : :   :   :   :   :   :   :
QY 139 GGF1FMGDV1HRMLTAIQYVAFLMANNREGYSDNSTVVYFDNGTVFVVQWDHVY-LQG  DD 233QRQYYVNQFKTIQPDLNGFIPGSAAKEFFTKSKLPILELSHIWELSD	IHKMLIAIQYVAFLMANNNEGYSDNSTVVYKDNGTVFVVQWDHVY-LQG 195 	Qy 247 NPSPDVPESRRSIFBYHRIELDPSKVT-SMSAVEFTPLPTCLQHRSCDACMSSDLTF 303
Qy 196 WEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNPS ::  :	IPMSVPEISSSQHPVKTGLSDAFMILNPS 249	304 NCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAE 335
Qy 250 PDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSMCH 	FTPLPTCLQHRSCDACMSSDLTFNCSWCH 309	DD 672 NVGWIYGSVTEDVVIGFRWHEKGWRSFYCVIEPD 705 RESULT 6
310 VLORCSSGFDR		S18606 phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49) - Rhizobium sp. C;Species: Rhizobium sp.
362 LNQS	IAPÁDPDTAIVHPVPIRMTPSKI	C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 27-Oct-2003 C;Accession: S18606
Qy 356YAGGDGLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNN	TKLNPYAGGDGLQNNLS 397  :  	R;Osteras, M.; Finan, T.M.; Stanley, J. Mol. Gen. Genet. 230, 257-269, 1991 A;Title: Site-directed mutagenesis and DNA sequence of pckA of Rhizobium NGR234, encodin
Qy 398 PKTKGTPVHLGT 409		A;Accession: S18606 A;Accession: S18606 A;Accession: Preliminary A;Catus: preliminary
DD 4.0 FEQUESSVIRGROUNGI 400		A;Molecule (ype: DNA A;Residues: 1-535 COST> A;Crose=references: EMBL:X63291 C.Sunerfamily. phosphoson  nvrnyste carbovykinses [ATD]
ABSOLI 3 C86446 probable cellulose synthase catalytic subunit	[imported] - Arabidopsis thaliana	C:Reywords: carbon-carbon lystuvace carboxy-lystuse (Air) C:Reywords: carbon-carbon lystuvace; carboxy-lystuse; nucleotide binding; P-loop F;234-241/Region: nucleotide-binding motif A (P-loop)
C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: C86446 B:Thaologis a Frker I B Dalm C I Bedereniel N a Kaul S White O	e88) -2001 #text_change 09-Jul-2004 exemiel N & . Kaul & . White O . Mloneo	Query Match 4.5%; Score 99; DB 2; Length 535; Best Local Similarity 20.7%; Pred. No. 3.5; Matches 59. Conservative 39. Manatches 117. Indels 70. Gans 12.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A. ansen, N.F.; Hudhes, B.; Huizar, L. Narine 408, 816-820, 2000	.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;	61 PDMRIAVEDNHSYXVSRLYGPSPEHSRELWUDAEANRSQVKIHTI-LSNTHR 1
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-C.A.; Li, J.H.; Li, X.; Lin, X.; Liu, S.X.; Li	-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. iu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,	86 PENFERLRODMLAHAKGMSLYVQDLVGAGQSGKCVADARRHRIRWHSLFIRNLLI
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shi ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter,	inn, P.; Southwick, A.M.; Sun, H.; Tallon,	OY 114 QASRVVLSPDFP-FYGHPLRQITIATGFIFWGDVIHR 150  141 RPPREGLASFLPKLTIIDLPSFRANPERHGCRGFIIACDLTKGLVLIGGTSYAGEMKKS 200
A,Title: Sequence and analysis of chromosome 1 A,Reference number: A86141; MUID:21016719; PMI A,Accession: C86446	l of the plant Arabidopsis. ID:11130712	
A;Status: preliminary A;Molecule type: DNA		
: 1-979 <sto> Ferences: UNIPROT:Q9FVR3;</sto>	GB:AE005172; NID:g10801364; PIDN:AAG23436.1; GSPDB:G	Qy 191 VYLQGWEDKGSFTFQAALHHDGRIVFAYKEIFMSVPEISSSQHPVKTGLSDAFMILNPSP 250
Query Match Query Match Best Local Similarity 21.1%; Pred. No. 6.1; Matches 83; Conservative 47; Mismatches	; DB 2; Length 979; .1; es 155; Indels 109; Gaps 19;	Qy 251 DVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDA 295 
QY 4 PQPCAGHDECPGSGWAAKGIVKGWNRRARESPGHVSEPDRTQLSQDLG	PGHVSEPDRTQLSQDLG 51	RESULT 7 T12529 hypothetical protein DKFZp434P113.1 - human (fragment)
Oy 52 GGTLAMDTLPDNRTRVVEDNHSYYVS  DD 414 GEGRALDLEGVDIRLPMLVYVS	TLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIH 105	C:Species: Homo Saptens (man) C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004 C:Accession: T12529 R;Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
106 TILSNTHR	1   1   1   1	submitted to the Protein Sequence Database, June 1999 A;Reference number: 217524 A;Accession: T12529
DD 459 AIMSNGPFILNLDCDHYVYNSKAF OY 158 VAPLMANFNPGYSD	GPFILMEDCDHYVINSKAFKDGICFMMDHDGDKVSYVQFPQKFEGID 510 NPQYSDNSTVVY-FDNGTVFVVQMDHVYLQG 195	A;Status: preliminary A;Nebidcule type: mRNA A;Residues: 1-1133 <wam></wam>
	GCLFRRTALYGFNPPDVFVVB 562	A;Cross-references: UNIPROT:Q9UG37; EMBL:AL080145 A;Experimental source: adult testis; clone DKFZp434P113 C;Genetics:

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corticosteroid-binding globulin precursor - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Decies: 31-Dec-1993 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004 C;Accession: S33415; 843740 B;Scrocchi, L.A.; Orava, M.; Smith, C.L.; Han, V.K.M.; Hammond, G.L. Bndocrinology 132, 903-909, 1993 A;Accession: Spatial and temporal distribution of corticosteroid-binding globulin and its me A;Reference number: S33415; MUID:93145908; PMID:7916682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-397 <SCR1>
A;Cross-references: UNIPROT:Q06770; EMBL:X70533; NID:g298114; PIDN:CAA49934.1; PID:g2981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                   :|| : | : | : | : : | : : | : : | TININGRVIDKTEEVANQAESIAINAMIKAVQ------SIKEGLSFLNVLYEESEV 919
                                                                                                                                                                                                                                                                                                                                                          44 TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVABANRSQVK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 IHTILSNTHRQASRVVLSFD-FPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAP-L 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MANFNPGYSDNSTVVYFD-----NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFEYHRIEL 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---APNDKTKSLIREILLSI 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRSQVKIHTILSNTHRQASRVVLSFDF-----PFYGHPLRQITIATGGFIFMGDVIHR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 FQAALHHD-----GRIVFAYKEIPMSVPEISSSQH-----PVKTGLSDAFMILNPSPDV 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 TGLEMNMGNVMFLLONLKLKDSFLADTKHYYESEALTIPSKD-----WTKAGEQINNHVK 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.Keywords: glycoprotein; steroid binding F;1-22/Domain: signal sequence #status predicted <SIG> F;1-22/Domain: signal sequence #status predicted <SIG> F:23-397/Product: corticosteroid-binding globulin #status experimental <MAT> F;89,169,217,232,253,320/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 NKTQGKIEHVVSDLDSSATLILINYIFLKGIWKLPFSPENTRE-------EDFYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----SKVSISKDCIEYY---LSSINILNEFFITYGDSI-----SQISAPYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              151 MLTATQYVAPLMANFNPGYSDNSTVV-----YFDNGTVFVVQWDHVYLQGWEDKGSFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAE-----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 397;
                                                                                                                                                                                                                                          DB 2; Length 1502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                  41; Mismatches 106; Indels
                        F;231-247/Domain: transmembrane #status predicted <TM1>F;434-450/Domain: transmembrane #status predicted <TM2>F;764-780/Domain: transmembrane #status predicted <TM3>F;1311-1327/Domain: transmembrane #status predicted <TM4>F;1312-1399/Domain: transmembrane #status predicted <TM4>F;1406-1423/Domain: transmembrane #status predicted <TM5>F;1406-1423/Domain: transmembrane #status predicted <TM5>F;1406-1423/Domain: transmembrane #status predicted <TM5>F;1406-1423/Domain: transmembrane #status predicted <TM6>F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 96.5; DB 2; I; Pred. No. 3.8; 47; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGFDNQYLGFKDİ-ISFVSLDVQKDLVKLDFKDLF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    971 INRNITKGASIEYT--ATALQERCGSFCSASDI 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDL 301
                                                                                                                                                                                                                                                                         Pred. No. 18;
                                                                                                                                                                                                                                          4.4%; Score 98; 22.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.4%;
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                                                                                                                                                                                                                                                                      Best Local Similarity 22.7%
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Molecule type: protein
A, Residues: 23-40 <SCR2>
C, Superfamily: Serpin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: S43740
                                                                                                                                                                                                                                                                                                                                                                                                                        778
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A;Cross-references: EMBL:X79489; NID:g496661; PIDN:CAA56029.1; PID:g496702
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 877 AIHKEDKENMNISGVEHPNGLEVIINTEİWDLRTFHLLHTVPALDQCRVVENHTGTVMYG 936
                                                                                                                                                                                                                                                                                                                                                                                                                        AFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTC-LQHRSCDACMSSD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : : | : | : | | : | | 337 AMLQADDEDDLMEERMKSPF------GSSFRTFNATDYKPIATIDVKRNIFDLCTD-- 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---AQEAEGRMCEDFQDEDH 347
                                                                                                                                                                                                                                                                                                  198 -----DKGSFTFQAALHHDGRIVFAYKEI------PMSVPEISSSQ---HPVKTGLSD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable membrane protein YBL079w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein YBL0725
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S45429; S45820; S45815; S59226
R;Obermaier, B.; Gassenhuber, J.; Piravandi, E.; Domdey, H.
submitted to the EMBL Data Library, May 1994
A;Description: Sequence analysis of a 78,6 kb segment of the left end of SacA;Reference number: S45387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: DNA
A;Residues: 1-1502 <0BE>
A;Cross-references: UNIPROT:P38181; EMBL:X79489; NID:g496661; PID:g496702
A;Experimental source: strain S288C
                                                                                                                                                                              145 GDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDNGTVFVVQWDHVYLQG--WE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-1502 < DDA>
A; Residues: 1-1502 < DDA>
A; Cross-references: BMBL: 235840; NID: 9536126; PID: 9536127; MIPS: YBL079w
A; Experimental source: strain S288C
B; Contreras, R.; Fiers, W.; Logghe, M.; Molemans, F.
B; Contreted to the Protein Sequence Database, August 1994
A; Reference number: $45802
A; Accession: $45815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1041 DEDDDDTD-----DLDELDTDQLLEAELEEDDN--NENAGEDG-DNDFSP 1082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSASPDTSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSP 398
                                                                                                                      68;
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A; Residues: 1262-1502 <CON>
A; Residues: 1262-1502 <CON>
A; Residues: 1262-1502 <CON>
A; Experimental source: strain $288C
A; Dermaler, B; Gassenhuber, J; Piravandi, E.; Domdey, H.
Yeast 11, 1103-1112, 1995
A; Title: Sequence analysis of a 78.6 kb segment of the left end of A; Reference number: $59184; MUID:96076635; PMID:7502586
A; Reference number: $59226
A; Status; nucleic acid sequence not shown; translation not shown
                                                     4.5%; Score 99; DB 2; Length 1133; 23.0%; Pred. No. 10; ive 37; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ದ.
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A;Accession: S45820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LTFNCSWCHVLQRCSSGFDRYRQEWMDYGC---
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A;Cross-references: SGD:S0000175; MIPS:YBL079w
A;Map position: 2L
                                                                                                                      Conservative
                                                                                    Similarity
A, Note: DKFZp434P113.1
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                                                                                                                   67;
                                                                                                                                                                                                                                                                                                                                                                                                                        242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348
                                                           Query Match
Best Local
                                                                                                                Matches
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11;

268

203

	Qy 115 ASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHR-	IGGFIFMGDVIHRMLTATQYVAPLMAN 164
Qy 253 PESRRRSIPEYHRIELDPSKV 273	Db 46 SSEIKLSVPFIFFRSPYRTVYVNN	:
Db 328 TKDTPLTLTVLHKAMLQLDEGNV 350		PNPGYSDNSTVVYFDNGTVFVVQMDHVYLQGWEDKGSF 202
	106	
RESULT 10 T19703	OV 203TFOAALHHDGRIVFAYKRIPMSVPRISSSOHPVKTGL	RIPMSVPEISSSOHPVKTGLSDA 242
hypothetical protein C34C12.2 - Caenorhabditis elegans C:Species: Caenorhabditis elegans	162	:   GGVMAOAGFNGGNISNF
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T19703	243	
K;KerBnaw, J. submitted to the EMBL Data Library, December 1994 A;Reference number: Z19166	Db 220 FSIPGSRTPDIVNIEQTINVNIPGRWAFKIDGREIDPANLS	
A;Accession: T19703 A;Status: preliminary; translated from GB/EMBL/DDBJ	RESULT 12	
A;Molecule Lype: DNA A;Residues: 1-679 eWIL> *.Crosq:	183196 NEDD-4 ORF - mouse (fragment)	
CONTRACTOR CONTRACTOR CONTRACTOR CONTRACTOR	Cibre: 02-Aug-1996 #sequence_revision C.Date: 02-Aug-1996 #sequence_revision	n 02-Aug-1996 #text_change 18-Aug-2000
	Rikumar, S.; Tomooka, Y.; Noda, M. Biochem. Biophys. Res. Commun. 185, 11	155-1161, 1992
605/3	A;Title: Identification of a set of ge A;Reference number: I60167; MUID:92328	enes with developmentally down-regulated expression 8780; PMID:1378265
Query Match 4.3%; Score 95.5; DB 2; Length 679; Best Local Similarity 24.4%; Pred. No. 9.6; No. 9.6; Gaps 12; Matches 65; Conservative 31; Mismatches 105; Indels 65; Gaps 12;	A;Accession: 183196 A;Status: preliminary; translated from A;Molecule type: mRNA	A,Accession: 183196 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: mRNA
SPCHVSEPDRTCH CALCETT AMDIT PRINTED NATIONAL SYCKES I WAS PRESENTED OF	A;Residues: 1-708 <res></res>	20508: PID: G220509
372 SPGPBGRTQISDQLNTGEVRYVVNSGKPFNFSSESNSRNLKLI 414	A/Genetics: A/Gene: NEDD-4	
ASRVVLSPDFPFYGHPLRQITIATGGFIFM 144	C,Superfamily: rat ubiquitin-protein l F;40-77/Domain: WW repeat homology <ww <<="" homology="" repeat="" td=""><td>ligase; protein kinase C C2 region homology; ubiqui Als. Ansos.</td></ww>	ligase; protein kinase C C2 region homology; ubiqui Als. Ansos.
Db 415 PGYIKRPBERYIKPEGFTSASYKAQSEGMSSFLKTGSSATPENSKKSAHFDM 466	F;150-23) Domain: www.repear.homology. F;251-282/Domain: www.repear.homology. F;347-682/Domain: ubiquitin-protein li	rmz> KWZ> KWZ> KWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CWZO V CZO V CZCO V CWZO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZCO V CZ
199	Query Match 4.3%; Score 95;	re 95, DB 2; Length 708;
10/ FUT031FINDINAVEDURINGOGSITGGE BSENNUNGARI103-000	1; Conservative 50;	Mismatches 150; Indels 180; Gaps 24;
OY COURTEQUALITH DEALTH TO THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL	ر د	
OY 260 IPEYHRIELDPSKVTSMSAVEFTPLP 285	DB 26 QPDAATHLPHPPEPSPLPFGWEEK	QPDAATHLEHEFEEVELEFGWEEKQDVLGKTYYVNHESKKTQWKKEVEFDDDIJDEDDDM 85
Db 563 RVEPISSSSGSTSTPRYVPKP 586		
RESULT 11 T30243	QY 86 HSRELWVDVAEANRSQVKIHTILS	86 HSRELWUDVAEANRSQVKIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGF 141 
alpha tectorin - chicken C.Sperjes. Gallus callus (chicken)	Db 138 HIDV	QTHLAEBENTRLAVCGNPATSQPVTSSNH 170
C;Decree: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004 C;Accession: T30243	OY 142 IFMGDVIHRMLTATOXVAPLM	IFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDNGTVFVVQWDHVYL 193
R;Coutinho, P.; Goodyear, R.G.; Legan, P.K.; Richardson, G.P. Hear. Res. 130, 62-74, 1999	Db 171 SSRĞGSLQTCIFEEQPTLPVLLPT	SSRĞGSLQTCIFEEQPTLPVLLPTSSGLPPCWEEKQDDRGRSYYVDHNSK-TTTWSKPTM 229
A;Title: Chick alpha tectorin : molecular cloning and expression during embryogenesis. A;Reference number: 220783; MUID:99251817; PMID:10320099	Qy 194 Q	QGWEDKGSFTFQAALHDGRIVFAYKEIPMSVPEI 228
A;Status: preliminary; translated from GB/EMBL/DDBJ	057	
A; Moleccule type: mRNA A; Residues: 1-2120 <cou> A; Cross-references: UNIPROT: O9YH85; EMBL: AJ012287; NID: e1361091; PID: e1361092; PIDN: CAAC</cou>	OY 229 SSSQHPVKTGLSDAFMILNPSPDV  :           Db 282 PRLQNVAITGPAV	SSSCHPVKTGLSDAFMILNPSPDVPESK KRSIFTSHKIELDPSKVISMSAVETITETIC 28/ 
llagenous protein only expressed in the inner (	QY 288 LOHRSCDACMSSDLTFNCSWCHVL	288 LOHRSCDACMSSDLTFNCSWCHVLORCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDE 345
Query Match 4.3%; Score 95.5; DB 2; Length 2120; Best Local Similarity 24.4%; Pred. No. 46; Matches 54; Conservative 28; Mismatches 72; Indels 67; Gaps 13;	Db 321 FBMK	: :     :    - lrraniledsyrr-imgykradllkarlwiefdgekg 360

24;

194

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A;Residues: 1-979 <LUJS-
A;Cross-references: UNIPROT:Q60673; EMBL:U11812; NID:g563737; PIDN:AAA52102.1; PID:g5637
A;Experimental source: brain
R;Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
submitted to the EMBL Data Library, June 1993
A;Description: Assessment of the expression levels of murine protein-tyrosine phosphatas
A;Reference number: $40280
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A; Residues: 801-837,839-852, 'T', 854-907 <HEN>
A; Cross-references: EMBL: Z23060; NID: 9438157; PIDN: CAA80595.1; PID: 9438158
A; Cross-references: EMBL: Z23060; NID: 9438157; PIDN: CAA80595.1; PID: 9438158
B; Magistralli, G.; Covinin, N.; Mosca, M.; Lippoli, G.; Isacchi, A.
B; Magistralli, G.; Covinin, N.; Mosca, M.; Lippoli, G.; Isacchi, A.
A; Magistralli, G.; Covinin, D.; Mosca, M.; Lippoli, G.; Isacchi, A.
A; Magistralli, G.; Covinin, D.; Mosca, M.; Lippoli, G.; Isacchi, A.
A; Title: Expression of PTP35, the murine homologue of the PTP2 se-related sequences 1A-2
A; Reference number: I48721; MUID: 9609562; PMID: 8526904
            protein kinase C C2 region homology; ubiqui
nomology <KC2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | : | : | : | : | CLOAHGAFITRRQISEDVDG-----PDNHESPENWEIVREDENTIYSGQAVQSPPSG 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | :: | :| : | | : | HP-DVQVRLAE-----ELDTRLT------MYGNPATSQPVTSSNHSSRG 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231 SQHPVKTGLSDAFMILNPSPDVPESR-RRSIPEYHRIELDPSKVTSMSAVEFTPLPTCLQ 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        531 MK--------LRRANILEDSYRR-IMGVKRADFLKARLWIEFDGEKGLD 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      381 GSSQTCIFEEQPTLPVLLPTSSGLPPGWEEKQDDRGRSYYVDHNSK-TTTWSKPTMQDDP 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35 --PGHVSEPDRTQLSQDLGGGTLAMDTLPDNRTR-----VVEDNHSYYVSR-LYGPSEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              146 DVIHRMLTATQYVAPLM----ANFNPGY----SDNSTVVYFDNGTVFVVQWDHVYLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            290 HRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDE---D
                                                                                                                                                                                                                                                                                                                                                       5 OPGAG----HDEGPG---SGWAAKGTVRG-------WNRRARES-----
                                                                                                                                                                                                                                                                                                                                                                                                               QPDAATHLQHPPEPSPLPPGWEERQDVLGRTYYVNHESRTTQWKRPSPEDDLTDDENGDI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 HDSASPD-----TSFSPYDGDLTTTSSSLFIDSLTTEDDT-KLNPYAG 388
                                                                                                                                                                                                                                                                                            Indels 175;
                                                                                                                                                                                                                                 Length 887;
                  C;Superfamily: rat ubiquitin-protein ligase; protein kinas F;54-167/Domain: protein kinase C C2 region homology «KC2>F;246-283/Domain: WW repeat homology «WW2>F;402-495/Domain: WW repeat homology «WW2>F;459-496/Domain: WW repeat homology «WW3>F;55-881/Domain: ubiquitin-protein ligase homology «UBI>
                                                                                                                                                                                                                                                                                            54; Mismatches 151;
                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                 4.2%; Score 93.5; 9.1%; Pred. No. 20;
                                                                                                                                                                                                                                                             19.1%;
                                                                                                                                                                                                               Query Match
Best Local Similarity 19.1%;
Warches 90; Conservative
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A;Residues: 1-887 <STA>
A;Cresidues: 1-867 <STA
A;Cresidues: UNIPROT:Q62940; EMBL:U50842; NID:g1293646; PIDN:AAB48949.1; PID:g129
C;Genetics:
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ubiquitin ligase Nedd4 - rat (fragment)

Uspecies: Rattus norvegicus (Norway rat)

C;Species: Rattus norvegicus (Norway rat)

C;Accession: 570642

R;Staub, O.; Dho, S.; Henry, P.C.; Correa, J.; Ishikawa, T.; McGlade, J.; Rotin, D.

R;Staub, O. 15, 2371-2380, 1996

A;Title: Ww domains of Nedd4 bind to the proline-rich PY motifs in the epithelial Na(+)

A;Reference number: S70642; MuID:96221297; PMID:8665844
                                                                                                                                                                                            neprilysin (EC 3.4.24.11) II - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 02-Sep-2000
C;Accession: JC7265
R;Tanja, O.; Facchinetti, P.; Rose, C.; Bonhomme, M.C.; Gros, C.; Schwartz, J.C.
Biochem. Biophys. Res. Commun. 271, 565-570, 2000
A;Title: Neprilysin II: A putative novel metalloprotease and its isoforms in CNS and A;Contents: Brain and testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: JC7265
A,Molecule type: mRNA
A,Residues: 1-774 <TAN>
C,Genetics: A,Genetics: C,Superfamily: neprilysin
C,Superfamily: neprilysin
C,Keywords: brain; glycoprotein; hydrolase; metalloproteinase; neuropeptide; testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -TOYVAPLMANFN-PGYSDNSTVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 RIVFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNPSPDVPESRRRSIFE-YHRIELDP- 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----SKVTSMSAVEFTPLPTCLQH-----RSCDACMSSDLTFNCS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 QERFGLKGFNWTLFIQNVLSSVQVELLPNEEVVVYGIPYLENLEEIIDVFPAQTLQNYLV 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WCHVLQRCSSGFDRYRQEWMDYGCA-----QEAEGRMCEDFQDEDHDSA------ 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 SEPLINVLDM-IGGWPVAMDKW--NET-------MGPKWELERQLAVLNSQFN 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSQVKIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTA---- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 SEPDRTQLSQDLGGGTLAMDTLPDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEAN 98
-DHDSASPD-----TSFSPYDGDLTTTSSSLFIDSLTTEDDTKLNPYAG 388
                                                    361 LDYGGVAREWFFLISKEMFNPYYG-----LFEYSATDNYTLQINPNSG 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.2%; Score 94; DB 2; Length 774;
21.3%; Pred. No. 15;
tive 44; Mismatches 123; Indels 136;
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Best Local Similarity
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A;Accession: 148721
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Resicule type: mRNA
A;Resicule type: mRNA
A;Resicule type: mRNA
A;Resicule type: mRNA
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A;Resicule type: mRNA
A;Resicule type: mRNA
A;Resicule type: mRNA
A;Resicule type: mRNA
A;Cross-references: EMBL:X74438; NID:g1089901; PIDN:CAA52453.1; PID:g1089902
C;Superfamily: protein-tyrosine-phosphatase, receptor type N; protein-tyrosine-phosphatase, receptor type N; protein-tyrosine-phosphatase, receptor type N #status predicted control F;38-979/Domain: extracellular #status predicted control type N #status predicted control F;577-598/Domain: intracellular #status predicted control control type N #status predicted control F;560-524/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;909/Active site: Cys (phosphocyateine intermediate) #status predicted
F;915/Inding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 RSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNC--SWC----- 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 -------HVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPD 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               687 MDISTGHMILAYMEDHLRNR-----DRLAKEWQAL-CAYQAEPNTCAAAQDESNIKKNRH 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Indels 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 4.2%; Score 93.5; DB 1; Length 979; Best Local Similarity 23.0%; Pred. No. 23; Matches 38; Conservative 23; Mismatches 55; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 TSFSPYDG-----DLTTTSSSLFIDSLTTEDDTKLNPYAGGDG 391
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SEQUENCE FROM N.A.
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(c) 1993 - 2005 Compugen Ltd.
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Q9h3q7 homo sapien Q9ukw9 homo sapien P4308 rhizobium s Q6urr8 xenopus la Q6urr8 xenopus la Q9gz22 homo sapien Q9gz22 homo sapien Q6pb14 brachydanio Aah5969 brachydan Q9f1t3 streptococc Q9fb48 corynebacte Q6pyv3 schistosoma Aas66224 schistosoo O68868 synechococc
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MEDLINE=21443268; PubMed=11559528;
MEDLINE=21443268; PubMed=11559528;
Kinzler E.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Romans K.E.,
Vogelstein B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-07-2001 (TrEMBLrel. 18, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last amocation update)
Tumor endothelial marker 7 precursor (Tumor endothelial marker
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tumor endothelial marker 3.
C545Al6619EEDBED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            St Croix B., Vogelstein B., Kinzler K.W.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ., Traverso G., ., Lengauer C.,
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100.0%; Pred. No. 4.2e-174;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                        500 AA
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                                         PPCK RHISN
QGURRB
AAQG2573
Q9H195
Q6PB14
AAH59696
Q9F1T3
Q9F1T3
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Cancer Res. 61:6649-6655(2001).
BMBL, AP279144, AAG00869.2; -.
BMBL, AP378753; AAL11990.1; -.
GO, GO:0001525; P:angiogenesis; NAS.
InterPro; IPR003659; Plexin-like.
InterPro; IPR02165; Plexin_repeat.
Ffan; PF01437; PS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20407466; Pubmed=10947988;
St Croix B., Rago C., Velculescu V.,
Montgomery E., Lal A., Riggins G.J.,
                                                                                                                                                                                                                     06PYV3
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinge; Mus.
NCBI_TaxID=10090;
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Carson-Walter B.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
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                                                                                                                                              99.9%; Score 2215; DB 2; Length 500; 99.8%; Pred. No. 7.5e-174; Live 1; Mismatches 0; Indels 0
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500 tumor endothelial marker 7.
55693 MW; 14FE25512A319DAF CRC64;
InterPro, IPR002165; Plexin_repeat.
Pfam; PF01437; PS1; 1.
SMART; SM00423; PS1; 1.
SEQUENCE 500 AA; 55778 MW; 3FA4F9D98A514ABF CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
11-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Name-Place and the marker 7 precursor.
Name-Place (Mouse)
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MGD; MGI:1919574; Plxdcl.
GO; GO:00046020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003165; Plexin_repeat.
Pfam; PF01437; PSI; 1.
SWART; SM00423; PSI; 1.
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WEDLINE=22386257; PubMed=12477932;

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B. B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

B Altschul R.F., Jordan H. B., Torbilyuki S.I., Wang J., Hong L.,

B Comnetein M.J., Usdin T.B., Toobilyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

B Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Mones S.J., Marra M.A.,

Shores S.J., Marra M.A.,

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Shores S.J
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                                      78 PDNRIRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 137
                                                                                                                           SPDFPFYGHPLROITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
                                                                                                                                                                                                                                                                                    GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS 257
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      PDNRTRVVEDNHSYYVSRLYGPSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVL 120
                                                                                                                                                                                     138 SFDFFPYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 197
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databages.
Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databages.
BMBL; 9306059, AM136059.1; -.
Genew; HGMC:20945; PLXDC1.
GO; GO:0004872; P:receptor activity; IEA.
GO; GO:000775; P:receptor activity; IEA.
InterPro; IPR003659; Plexin-like.
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                                                                                             DAFMIINSSPEVPESQRRIIFEYHRVELDSSKITTTSAVEFTPLPTCLQHQSCDTCVSSN 318
                                                                                                                                                                                                                                                      LIFNCSWCHVLQRCSSGFDRYRQEWLTYGCAQEAEGKTCEDFQDDSHYSASPDSSFSPFN 378
                                                                                                                         SFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDN 180
                                                                                                                                                                GTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLS 240
                                                                                                                                                                                                     DAFMILNPSPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSD 300
                                                                                                                                                                                                                                           LIFNCSWCHVIQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPDISFSPYD 360
                                                               78
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                                                        ALSPQPGAGHDEGPGSGWAAKGTVRGWNRRARESPGHVSEPDRTQLSQDLGGGTLAMDTL
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
"Functional annotation of a full-length mouse cDNA collection.";
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone: 3410013107 product: TUMOR ENDOTHELIAL MARKER 7 homolog.
                            1;
          Length 500;
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         9.5; DB 2
1.3e-139;
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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          81.1%; Score 1799.5;
80.7%; Pred. No. 1.3e
ive 39; Mismatches
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MEDLINE=99279253; PubMed=10349636;
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Mammalia; Butheria; Rodentia;
NCBI_TaxID=10090;
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                             Conservative
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Bubi, MGI: 1919574; Plxdcl.

GO: GO:0016020; C:membrane; IEA.

GO: GO:001275; Fireceptor activity; IEA.
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        Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Moralization and subtraction of cap-trapper-selected cDNAs trappere full-length CDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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80.9%; Score 1793.5; DB 2;
Best Local Similarity 80.5%; Pred. No. 4.2e-139;
Matches 330; Conservative 39; Mismatches 40;
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Interpro, IPR003659; Plexin-like.
Interpro, IPR002165; Plexin_repeat.
                                                                                                                                                                                                          STRAIN=C57BL/6J;
MEDLINE=20530913; PubMed=11076861;
MEDLINE=20499374; PubMed=11042159;
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NCBI_TaxID=9606;
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LTFNCSWCHVLQRCSSGFDRYRQEWLTYGCAQEAEGKTCEDFQDDSHYSASPDSSFSPFN 378
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STRANTE-S7BL/GJ; TISSUE=Cerebellum;
STRANTON CONSORTIUM;
The FANTOM CONSORTIUM;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
whallysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MEDLINE=20499374; PubMed=11042185;
Carninci P., Shibata UY., Hayatsu M., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630 (2000).
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                                                                                                                                                                                                                                               01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length
enriched library, clone:9630040L07 product:TUMOR ENDOTHELIAL MARKER
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MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsunnoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Nohazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RIKKN integrated sequence analysis (RISA) system-384-format
Sequencing pipeline with 384 multicapillary sequence:";
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Sciurognathi; Muridae; Murinae; Mus
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
                                               410
                                                                    GD-STISSSLFIDSLITEDDIKLNPYAEGDGLPDHSSPKSKGPPVHLGTI
                                            GDLTTTSSSLFIDSLTTEDDTKLNPYAGGDGLQNNLSPKTKGTPVHLGTI
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MEDLINE=99279253; PubMed=10349636;
Carninol P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MEDLINE-2108566; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
                                                                                                                                                                                                      PRT;
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
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319 DTCVSSNLTFNCSWCHVLQRCSSGFDRYRQEWLTYGCAQEAEGKTCEDFQDDSHYSASFD 378
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Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Kathara K., Kojima Y., Kondo B., Konno H., Kouda M., Koya S. Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki Y., Sogabe Y., Tagawi D., Shibata K., Takaku-Akahira S., Takeda Y., Tanaka T., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00423; PSI; 1.
C2D50B44561C3415 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 80.3%; Score 1780; DB 2; Best Local Similarity 79.1%; Pred. No. 5.5e-138; Matches 330; Conservative 39; Mismatches 40;
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                                                                                                                                                                                                                                                                                                            MGD; MGI:1919574; Plxdcl.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR007100; Ig-like.
InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
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Homo sapiens (Human).
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SMART; SM00423; PSI
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258

188 198 308

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SPDVPESRRRSIFEYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWC
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                                                                                                                                                           DHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNP
                                                                                                                                                                               DHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQHPVKTGLSDAFMILNP
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                                                                                       HPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFDNGTVFVVQW
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Bioinformatics assessment.";

EMBL, AV358486; AQ68850.1; -.

InterPro; IPR003559; Plexin-like.

InterPro; IPR003559; Plexin-like.

InterPro; IPR01431; PSI; 1.

SMART; SM04423; PSI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            529 AA; 59583 MW; CCE911D6DF837B40 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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HVLQRSLNNQD 329
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                                                                                                                                                                                                                                PGSGWAAKGTVRGWNRRARESPGH-----VSEPDRTQLSQDLGGGTLAMDTLPDNRTRVV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAC87025 PRELIMINARY; PRT; 351 AA.
BAC87025;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2014 (TrEMBLrel. 27, Last annotation update)
CDNA RL45632 fis, clone CHONS2001834, highly similar to Homo sapiens tumor endothelial marker 7 (TEM7).
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Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K.,
Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.,
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                                                                                                                                                                                               22;
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Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; Submitteed (JUL-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AK127539; BAC87025.1; -
InterPro; IPR001265; Plexin_repeat.

Pfan; PF01437; PSI; 1.

SEQUENCE 351 AA; 39639 MW; FE03CC9D78E4604A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK127539; BAC87025.1;
SEQUENCE 351 AA; 39639 WW; FE03CC9D78E4604A CRC64;
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                                                                                                                                                             59.8%; Score 1326; DB 2;
82.6%; Pred. No. 8.8e-101;
iive 4; Mismatches 28;
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257; Conserv
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                           215 TVRYFDNGTALVVQMDHVHLQDNYNLGSFTFQATLLMDGRIIFGYKEIFVLVTQISSTNH
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DACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPD
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Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Clark H.F., Gurney A.L., Abaya E., Currell B., Dauel B., Dowd P., Chen J., Chow B., Chul C., Crowley C., Currell B., Dauel B., Dowd P., Eaton D., Krim H.S., Klimwaski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
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SEQUENCE 529 AA; 59583 MW; CCE911D6DF837B40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                 529
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                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel.
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tes 205; Conserv
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SEQUENCE FROM N.A.
                                                                                                                                                                                           GTI 410
                                                                                                                                                                                                                                          GLI 457
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                                                                                                                                                                                                                 T--SFSPYDGDLTTTS---SSLFIDSLTTEDDTKLNPYAGGDGLQ-NNLSPKTKGTPVHL 407
                                                                                                                                                                                                                                               QASRVVLSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TVVYFDNGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPEISSSQH 233
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                                                                                                                      DACMSSDLTFNCSWCHVLQRCSSGFDRYRQEWMDYGCAQEAEGRMCEDFQDEDHDSASPD 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and

    30 Potential.
    529 tumor endothelial marker 7-related.
    529 AA; 59583 MW; D44A0975DF894840 CRC64;

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MEDIJNE=21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St. Croix B.;
"Cell surface tumor endothelial markers are conserved in mice."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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01-OCT-2003 (TrEMBLrel. 25, Last annotation u
Tumor endothelial marker 7-related precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     529 AA
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0004972; P:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR003659; Plexin_like.
InterPro; IPR003659; Plexin_repeat.
Ffam; PF01437; PSI; 1.
SWART; SM00423; PSI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cancer Res. 61:6649-6655(2001).
EMBL; AF378757; AAL11994.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
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(TrEMBLrel. 19, L
(TrEMBLrel. 25, L
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Best Local Simil
Matches 205; (
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Name=Plxdc2;
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SEQUENCE FROM N.A.

STRAIN-NMRI; TISSUE-Mammary tumor. WAP-Tag model. 5 months old;

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul, S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul, S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 WKRNV--DPFKAVDINRASMGQASPESKGFIDLLLDDGQDNNTQIEEDTDHNYYISRIYG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27 WNRRARESPGHVSEPDRTQLSQ----DLGGGTLAMDTLPDNRTRVVED-NHSYYVSRLYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.1%; Score 1044; DB 2; Length 530;
51.3%; Pred. No. 2.7e-77;
ive 67; Mismatches 112; Indels 14; Gaps
                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=NWRI; TISSUE-Mammary tumor. WAP-Tag model. 5 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stransberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC057881; AAHS7881.1; -
InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
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SPART; SM00423; PSI; 1.
SROUBNCE 530 AA; 59646 MW; D7256C02073417FC CRC64;
                                                                                                                                  (TrEMBLrel. 27, Last sequence update) (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                           530 AA
                                                                                                                    Created)
                                                                                          PRT;
                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Last an
Tumor endothelial marker 7-related,
                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
                                                                                                                    (TrEMBLrel. 27,
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Best Local Similarity 51.37
Best Local Similarity 51.37
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences.
                                                                                          PRELIMINARY;
                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                              NCBI_TaxID=10090;
                         457
 GTI 410
                         GLI
                                                                                                                                                                          Name=Plxdc2;
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408
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Q6PETS
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375
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                                           STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oĘ
                                                                                                                                                                                                                         363 RÓDWVDSGCPEEVQSKEKMCEKTEPGETSQTTTTSHTTTMQFRVLTTTRRAVTSQMPTSL
EYHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRY
                                                                                                                                                  RQEWMDYGCAQEAEG--RMCEDFQDEDHDSASPDTSFSPYDGDLTTTS----SSLFIDSL
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=tung;
SETRAIN=C57BL/6J; TISSUE=tung;
SEDIINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
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MEDLINE=21085660; PubMed=11217851;
RIKEN PATOM CONSORTIUM;
"FULLCIONAL AMDOLATION of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone:1200007L24 product:TUMOR ENDOTHELIAL MARKER 7-RELATED
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MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
Clarinci P., Hayashizaki Y.;
Migh-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Lung;
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SEQUENCE FROM N.A.
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 NCBI_TaxID=10090;
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                   SEQUENCE FROM N.A.

Adachi J., Aizawa K., Akhinza S., Akimura T., Arai A., Aono H.,

Adachi J., Aizawa K., Akhira S., Akimura T., Arai A., Aono H.,

Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

A Arakawa T., Bahon H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

Asano H., Sasaki D., Shibata K., Shibata Y., Saki K.,

Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

A Fojima Y., Zohido T., Vamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.,

Submitted (UUL-2000) to the BMBL/GenBank/DDBJ databases.

B MGD, MGI:1914698; Plxdc2.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

R GO; GO:0004872; F:receptor activity; IEA.

R InterPro; IPR008941; PLC Nuclease.

R InterPro; IPR008959; Plxdc1-like.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2004 (TrEMBLrel. 19, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Tumor endothalial marker 7-related precursor.
Name-Plxdc2; Synonyms-Tem7R;
Nume musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musnae.
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47.1%; Score 1044; DB 2; Length 530;
Best Local Similarity 51.3%; Pred. No. 2.7e-77;
Matches 203; Conservative 67; Mismatches 112; Indels 14;
                                                                                                                                                                                                                                                                                                   InterPro; IPR002165; Plexin_repeat.
Pfam; PF01437; PSI; 1.
SWART; SM00423; PSI; 1.
SEQUENCE 530 AA; 59616 MW; PB956C020735E36D CRC64;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 30 Potential.
31 530 tumor endothelial marker 7-related.
530 AA; 59625 MW; FF8315020735B36D CRC64;
MEDLINE=21443268; PubMed=11559528;
Cargon-Walter B.B., Warkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'Match 47.1%; Score 1044; DB 2; Length 530; Local Similarity 51.3%; Pred. No. 2.7e-77; les 203; Conservative 67; Mismatches 112; Indels 14
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02-WAR-2004 (TrEMBirel. 27, Created)
02-WAR-2004 (TrEMBirel. 27, Last sequence update)
02-WAR-2004 (TrEMBirel. 27, Last annotation update)
Tumor endothelial marker 7-related.
Mus musculus (Mouse).
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MGD; MGI:1914698; Plxdc2.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; P:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR003659; Plexin-like.
InterPro; IPR001655; Plexin_repeat.
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SMART; SM00423; PSI; 1.
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Altschul S.F., Zeeberg B., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bronstein M.J., Uddin T.B., Toshiyuki S., Carninof P., Prange C., Bran S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Ganzatne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzuey C.M., Sdergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Bhakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., M. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           PSEPHSRELWVDVAEANRSQVKIHTILSNTHRQASRVVLSFDFPFYGHPLRQITIATGGF 141
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                                                                                                                                                                                        Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
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Kenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopus.

NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                         Length 530;
                                                                                                                                                                                                                                                                                                                                        47.1%; Score 1044; DB 2; Length 5
51.3%; Pred. No. 2.7e-77;
ive 67; Mismatches 112; Indels
                                                                                                                                                                                                                                                                           Strausberg R., Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                    EMBL; BC057881; AAH57881.1; -.
SEQUENCE 530 AA; 59646 MW; D7256C02073417FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 28, Last sequence update) (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
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STRAIN=NMRI; TISSUE=Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 28, (TrEMBLrel. 28,
                                                                                                                                                                                                                  and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                  Matches 203; Conservative
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A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Antechnic L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Socres M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McKwan P.J., McKernan K.J., Malte J.A., Gunzarene P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                             "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   46.6%; Score 1034.5; DB 2; Length 513; llarity 51.3%; Pred. No. 1.6e-76; Conservative 69; Mismatches 106; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klein S., Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC077242; AAH77242.1; -.
Hypothetical protein.
SEQUENCE 513 AA; 57622 MW; 301EAS3F2905A4ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                      Dev. Dyn. 225:384-391(2002).
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Search completed: January 28, 2005, 22:11:23 Job time : 141.695 secs

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Q6pyv2 schistosoma Aas68255 schistoso P51805 homo sapien Q9uiw1 homo sapien Q76915 bos taurus Bad05055 bos tauru

musculu schistosoma

Q8c3x9 Q8cgw1 09qzc2 Q86e23 homo sapien mus musculu xenopus lae trichinella

075051 P P70208 P Q91823 P 06ybw0

Title: Perfect score:

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protein

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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**X TASUBE-1288118;

**X TASUB-1288118;

**X MEDLINE=22388257; PubMed=12477932;

**X KINDELINE=22388257; PubMed=12477932;

**X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

**X Altschul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhat N.K.,

**A Altschul S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Haieh F.,

**A Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

**A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

**A Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

**A Bosak S.A., McKwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,

**A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

**A Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

**A Nhiting M., Madan A., Young A.C., Shevchenko Y., Buitfard G.G.,

**A Rodriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

**A Rodriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

**A Nones S.J., Marra M.A.,

**Jones S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                            Ol-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Plexin domain containing 1,.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                   Q6PYV2
AAS68255
PLX4 HUMAN
Q9UIW11
                                                                                                                                          Q76915
BAD05055
O75051
P70208
Q91823
Q6YBW0
                                                                                                                                                                                                                                                                                                                                                                                PRT;
                  Q8CGW1
Q9QZC2
Q86E23
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                                                                     343
343
1871
1328
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1905
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SMART; SM00423; PSI; 1
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 28 IUKS
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O6486 homo sapien
Q742j8 anopheles g
Q8cjh3 mus musculu
O45657 caenorhabdi
CabO5755 caenorhab
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q6ux71 homo sapien
Q96pd9 homo sapien
Aaq88850 homo sapi
Q6de92 xenopus lae
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Bac87025 homo sapi
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Aah66773 homo sapi
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1688.701 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       xenobna
                                                                                                                         January 28, 2005, 21:55:21 ; Search time 22.1468 Seconds
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                  GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                           1825181 segs, 575374646 residues
                                                                                                                                                                                                US-09-918-715-230_COPY_280_344
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Maximum Match 100%
Listing first 45 summaries
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06BM20
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Q18500
G60486
Q7Q2J8
Q8CJH3
Q45657
CABO5755
Q6DCPO
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Gapop 10.0 , Gapext 0.5
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  2: uniprot_trembl:*
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seq length: 200000000
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Match Length DB
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-007-2001 (TrEMBLrel. 18, Last sequence update)
05-0UL-2004 (TrEMBLrel. 27, Last annotation update)
Tumor endothelial marker 7 precursor (Tumor endothelial marker
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St Croix B., Rago C., Velculescu V., Traverso G., Romans K.E.
Montgomery E., Lal A., Riggins G.J., Lengauer C., Vogelstein
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Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
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tumor endothelial marker 3.
C545A16619EEDBED CRC64;
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St Croix B., Vogelstein B., Kinzler K.W.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
     Pred. No. 3.3e-35;
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100.0%; Pred. No. 3.3e-35;
iive 0; Mismatches 0;
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EMBL, AF379753; AAL11990.1; -
GO; GO:0001525; P:angiogenesis; NAS.
InterPro; IPR003569; Plexin-like.
InterPro; IPR003165; Plexin_repeat.
Pfam; PF01437; PSI; 1.
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100.0%;
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                             65; Conservative
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Similarity
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RESULT Q9CWV5

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the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shibata K. Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K. Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Akiyama J., Nishi K., Kitama M., Nishino H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Tagawa M., Ohara B., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., Rikik integarated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21085660; PubMed-11217851;
RIKEN FANYOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone: 2410003107 product:TUMOR ENDOTHELIAL MARKER 7 homolog.
                                                                                                                                                                                                                                                                                                                        Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
  500 AA.
PRT;
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MEDLINE=20499374; PubMed=11042159;
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  PRELIMINARY;
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Nature 420:563-573(2002)
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Q9CWV5;
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RESULT 5
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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MEDLINE=21443268; PubMed=11559528;
MEDLINE=2144326B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
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ive 7; Mismatches 3; Indels
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MGD; MGI:1919574; Plxdcl.
GO; GO:10016020; C:nembrane; IEA.
GO; GO:0004712; F:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR00710; Ig-like.
InterPro; IPR003165; Plexin_like.
InterPro; IPR003165; Plexin_like.
InterPro; IPR003165; Plexin_repeat.
SMART; SM0437; PSI; 1.
SMART; SM0437; PSI; 1.
SEQUENCE 500 AA; 55635 MW; 802D6865F8CA18BD CRC64;
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MGD; MGI:1919574; Plxdci...

GO; GO:0004872; F:receptor activity; IBA...

GO; GO:0007275; P:development; IEA...

InterPro; IPR003710; IG-like...

InterPro; IPR003165; Plexin-repeat...

Pfam; PF01437; PSI: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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EMBL; AF378760; AAL11997.1; -.
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500 AA;
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01-DEC-2001
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Best Local
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10012V7
10012V7
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ESQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Cerebellum;

STRAIN=C57BL/6J; TISSUE=Cerebellum;

MEDLINE=20530913; PubMed=11076861;

A Shibatea K., Itch M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Akiyama J., Alzawa K., Kitsunai T., Tashiro H., Itch M., Sumi N., Ishlii Y., Nakamura S., Hazama M., Nishline T., Harada A., Sumi N., Ishlii Y., Nakamura S., Izawa M., Ohara E., Watshiki M., Pujiwake S., Innoue K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Arakiki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN Integrated sequence analysis (RISA) system=384-format sequencing pipeline with 384 multicapillary sequencer.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MUS musculus 16 days neonate cerebellum CDNA, RIKEN full-length
enriched library, clone:9630040L07 product:TUMOR ENDOTHELIAL MARKER
                                                                                                                                                                                                                                                                                                                                                                                                 Name=Pīxdc1;
Nam musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUB=Cerebellum,
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium,
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
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MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
Hitch-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
          507 AA.
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STRAIN-C57BL/6J; TISSUE-Cerebellum;
The FANTOM Consortium,
PRT;
               PRELIMINARY;
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sapiens (Human)
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QGPET5
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Oshima A., Takahashi-Pujii A., Tanase T., Imose N., Takeuchi K.,

A Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,

Otsuki T., Sato H., Wakamateu A., Imabayashi H.,

A Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,

A Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K.,

Nakamura Y., Sekine M., Kikuchi H., Kanda K., Waqatsuna M.,

Murakawa K., Sarhori K., Sugiyama A., Kawakami B., Suzuki Y.,

Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;

Submitted (JUL-203) to the Embl/GenBank/DDBJ databases.

EMBL, AK127539, BAC87025.1; -.

EMBL, AK127539, Plexin_repeat.

Pfam; PF04437; PS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2002 (TrEMBLrel. 27, Last annotation update)
CDNA FLJ45632 fis, clone CHONS2001834, highly similar to Homo sapiens tumor endothelial marker 7 (TEM7)
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                                                                                                                                                                                                   Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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                                   MGD; MGT:191574; Plxdc1.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0007775; P:development; IEA.

InterPro; IPR007110; Ig-like.

InterPro; IPR003165; Plexin-like.

InterPro; IPR01655; Plexin-like.

InterPro; IPR0165; Plexin-repeat.

Pfam; PF01477; PS1; 1.

SMART; SM00423; PS1; 1.

SEQUENCE 507 AA; 56332 MW; C2D50B44561C3415 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                  05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein FL745632.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.6%; Score 287; DB 2;
91.2%; Pred. No. 1.5e-25;
iive 1; Mismatches 4;
                                                                                                                                                                        87.8%; Score 325; DB 2;
84.4%; Pred. No. 6.9e-30;
ive 7; Mismatches 3
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Best Local Similarity
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Best Local
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=NMRI; TISSUE=Mammary tumor. WAP-Tag model. 5 months old;

Kausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.P., Zeeberg B. Buetow K.H., Schemen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

Altschul S.P., Zeeberg B., Buetow K.H., Schemen C.M., Schetz T.B.,

By Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A trapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Usdin T.B., Toebilyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., McKwan P.J., McKernan R.J., Malek J.A., Gunarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahebley J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rahebley M., Helton B.K., Green E.D., Dickson M.C.,

Rahebley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A dones S.J., Marxa M.A.,

"Mandan A., Schein E.D., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 YHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLFFNCSWCHVLQRSLNNQD 329
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                                                                                                                                                                                                          Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H., Fukuma M., Hata J., 1shii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nahikawa Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human cDNA sequencing project."; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Bukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.6%; Score 287; DB 2; Length 35
91.2%; Pred. No. 1.5e-25;
tive 1; Mismatches 4; Indels
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Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AK127539; BAC87025.1; -.
SEQUENCE 351 AA; 39639 MW; FE03CC9D78E4604A CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
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                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRANT-CS7BL/GJ; TISSUB=Lung;
STRANT-CS7BL/GJ; TISSUB=Lung;
The FANTOM CONSOrtium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200007L24 product:TUMOR ENDOTHELIAL MARKER 7-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CS7BL/6J; TISSUE=Lung;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                           1 YHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYR
                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata, Vertebrata, Euteleostomi,
Sciurognathi, Muridae, Murinae, Mus.
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STRAIN=C57BL/6J; TISSUB=Lung;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORtium;
"Functional annotation of a full-length mouse cDNA collection.";
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0
                                                                                                        Length 530;
                                                                                                                                                        12; Indels
Pfam; PF01437; PSI; 1.
SMART; SM00423; PSI; 1.
SEQUENCE 530 AA; 59646 MW; D7256C02073417FC CRC64;
                                                                                                     71.4%; Score 264; DB 2; 67.7%; Pred. No. 1.2e-22; ive 9; Mismatches 12
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MEDLINE=99279253; PubMed=10349636;
Carninol P., Hayashizaki Y.,
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                        44; Conservative
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364 QDWVD 368
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                                                                                                        Query Match
Best Local
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STRAIN-C57BL/63; TISSUE-Lung;
Adachi J. Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Cazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Takahashi F., Tanaka T.,
A Fejima Y., Toya T., Yamamura T., Yasunishi A., Yoshino M.,
Muramatsu M., Hayashizaki Y.;
Bubi Akookato, Babilali Y., Shibank/DDBJ databases.
Bubi Akookato, Babilali I., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., Fulli F., 
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MEDIJNE=21443268; PubMed=11559528;
MEDIJNE=21443268; PubMed=11559528;
Karson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
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Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR008947; PLC_Nuclease.
InterPro; IPR003659; Plexin-like.
InterPro; IPR003659; Plexin_repeat.
Pfam; PF01437; PSI; 1.
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007275; P:devalopment; IEA.
InterPro; IPR003659; Plexin_repeat.
InterPro; IPR002165; Plexin_repeat.
Pfam; PF01437; PSI; 1.
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Cancer Res. 61:6649-6655(2001).
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Mus musculus (Mouse).
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Matches 44; Conservative
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ODWVD 319
364 QDWVD 368
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                                                                                                        NCBI_TaxID=9606;
                                                                          PLXDC2 protein.
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                                             296E59;
01-DEC-2001
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                      RESULT 12
Q96E59
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                                                                          1 YHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCSSGFDRYR
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                                                           Gaps
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                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                     tumor endothelial marker 7-related. FF8315020735E36D CRC64;
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                                             Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.4%; Score 264; DB 2; Length 53(67.7%; Pred. No. 1.2e-22; ive 9; Mismatches 12; Indels
                                            71.4%; Score 264; DB 2; Length 53 67.7%; Pred. No. 1.2e-22; ive 9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-NWRI; TISSUE-Mammary tumor;
Strausberg R.;
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; BC057881; AAH57881.1; -.
SEQUENCE 530 AA; 59646 MW; D7256C02073417FC CRC64;
                                                                                                                                                                                   02-MAR-2004 (TrEMBLrel. 27, Last sequence update) 02-MAR-2004 (TrEMBLrel. 27, Last annotation update) Tumor endothelial marker 7-related.
                                                                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                              530 AA
                Potential.
                                                                                                                                                                            02-MAR-2004 (TrEMBLrel. 27, Created)
                     530 to 59625 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 67.7
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.
                                                           44; Conservative
                                                                                                                                                             PRELIMINARY;
SMART; SM00423; PSI; 1.
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31 5
530 AA;
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                                            Query Match
Best Local Similarity
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                                                                                                         61 QEWMD 65
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                     CHAIN
SEQUENCE
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AAH57881;
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XX MEDINE-2248825;

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XI strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

XI strausberg R.L., Feingold B.A., Grouse L.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B. Buetcw K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Antschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Antschul R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Antschul S.J., Marsen M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012885; AAH12885.1; -.
EQC) GO:00164872; Cimembrane; IEA.
GO; GO:0004872; Fireceptor activity; IEA.
GO; GO:0007275; Pidevelopment; IEA.
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CE 480 AA; 53912 MW; F8DB0E2631BC7816 CRC64;
                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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   480 AA
   PRT;
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InterPro, IPR002165, Plexin_repeat
Edm, PF01437, PSI, 1.
SMART, SM00423, PSI, 1.
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Best Local Similarity 67.7'
Matches 44; Conservative
PRELIMINARY;
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Godowski P.;
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  Signal.
SIGNAL
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                                                                                                                                                                                                                                         Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Sainth V., Stinson J., Wagts A., Vandlen R., Watenabe C., Wark M., Robbie E., Santh V., Stinson J., Wagts A., Vandlen R., Watenabe C., Waisand D., Woods K., Xie M.H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment.";
Genome Res. 13:2265-2270 (2033).
EMBL; AY358486; AAQ88850.1; -..
InterPro; IPR0031659; Plexin-like.
InterPro; IPR001555; Plexin-like.
Pfem; PR01437; PSI; 1.
                                                                                  Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE-1443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.1%; Score 263; DB 2; Length 52
67.7%; Pred. No. 1.5e-22;
ive 9; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    529 AA; 59583 MW; CCE911D6DF837B40 CRC64;
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Tumor endothelial marker 7-related precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    humans.,;
Cancer Res. 61.6649-6655(2001).
BMBL; AR378757; AAL11994.1; -..
Genew, HGNC:21013; PLXDC2.
GO; GO:0004872; P:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR003659; Plexin-like.
InterPro; IPR003655; Plexin-repeat.
Pfam; PF04437; PSI; 1.
SMART; SM00423; PSI; 1.
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MEDLINE=22887296; PubMed=12975309;
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                                                                        Homo sapiens (Human).
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                                                 ORFNames=UNQ2514;
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Q96PD9
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DT O1-DE DT O1-DE DT O1-DE DT O1-OE
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                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
30 Potential.
529 tumor endothelial marker 7-related
59583 MW; D44A0975DF894840 CRC64;
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                                                                                                               Length 529;
                                                                                                                                                                12; Indels
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Pred. No. 1.5e-22;
9; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                529 AA.
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11.1%;
Best Local Similarity 67.7%;
Matches 44; Conservative 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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31 5
529 AA;
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PubMed=12975309;
                                                                                                                                                                                                                                                                                                                                                                                         364 QDWVD 368
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January 28, 2005, 21:55:58 ; Search time 4.50139 Seconds (without alignments) 1389.370 Million cell updates/sec Run on:

370 1 YHRIELDPSKVTSMSAVEFT......CHVLQRCSSGFDRYRQEWMD 65 US-09-918-715-230\_COPY\_280\_344 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pirl:\* 2: pir2:\* 3: pir3:\* 4: pir4:\* PIR\_79:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		de			SUMMAKIES	
Result No.	Score	Query Match	Query Match Length	DB	QI	Description
11111						
Н	137	37.0	476	7	T19786	hypothetical prote
7	101	27.3	1568	7	T09074	semaphorin recepto
٣	84	22.7	1806	7	T23298	hypothetical prote
4	77.5	20.9	1872	7	JC4976	plexin 3 precursor
'n	76.5	20.7	1905	7	151553	
9	16	20.5	1884	~	JC4975	~
7	75	20.3	1945	~	T13937	plexin A - fruit f
80	74	20.0	Н	~	JC4980	
о	70	18.9	1379	-	S01254	hepatocyte growth
10	69.5	18.8		~	D88448	protein C45G9.8 [i
11	69	18.6		7	G84565	probable flavonol
12	68	18.4	_	٦	TVHUME	hepatocyte growth
13	67.5	18.2	1375	7	T30813	plasminogen relate
14	67.5	18.2		~	T13164	plexin B - fruit f
15	67	18.1		7	G81349	periplasmic nitrat
16	67	18.1		Н	JC5148	hepatocyte growth
17	65	17.6	1425	~	T30811	hepatocyte growth
18	64.5	17.4		7	H75070	sugar-phosphate nu
19	64.5	17.4		7	T21694	hypothetical prote
20	64	17.3		7	H84565	probable flavonol
21	63.5	17.2	846	~	A30889	integrin beta chai
22	63	17.0	1404	ч	A48196	protein-tyrosine k
23	62.5	16.9	439	~	S33293	testican - human
24	62.5	16.9		7	S31784	VP5 protein - bovi
25	62.5	16.9		7	T27165	hypothetical prote
56	62.5	16.9		~	G71308	probable aminopept
27	62.5	16.9	_	~	T16169	hypothetical prote
28	61	16.5	210	~	S76973	hypothetical prote
59	61	16.5	m	7	T42761	Bassoon protein -

30 61 16.5 3942 2 T42730 31 60 16.2 90 2 S70194 32 60 16.2 248 2 T16642 34 59.5 16.1 513 2 T35512 35 59.5 16.1 543 2 S6450 37 59.5 16.1 1819 2 E86410 38 59.5 16.1 1819 2 E86410 40 59 15.9 338 2 T26588 40 59 15.9 555 2 T26588 41 58.5 15.8 311 2 S08110 42 58.5 15.8 312 2 R6842 44 58.5 15.8 346 2 R6882 44 58.5 15.8 416 2 A71095	Bassoon protein -	hypothetical prote	hypothetical conse	hypothetical prote	hypothetical prote	probable membrane	protein-tyrosine k	protein F3M18.14 [	hypothetical prote	probable SET-domai	hypothetical prote	salivary protein 1	probable zinc fing	hypothetical prote	probable sugar-pho	probable C2H2-type
61 16.5 60 16.2 60 16.2 60 16.2 60 16.2 59.5 16.1 59.5 16.1 59.5 16.1 59.5 16.1 59.5 15.9 58.5 15.9 58.5 15.8 58.5 15.8 58.5 15.8 58.5 15.8	T42730	S70194	E95974	T16642	T33512	S64850	T30200	E86410	T26588	T00834	T23531	808110	B86382	T08345	A71095	A84431
61 16.5 60 16.2 60 16.2 60 16.2 60 16.2 59.5 16.1 59.5 16.1 59.5 16.1 59.5 16.1 59.5 15.9 58.5 15.9 58.5 15.8 58.5 15.8 58.5 15.8 58.5 15.8	7	~	0	~	N	N	0	~	7	~	7	N	~	N	N	7
61 61 61 61 61 61 61 61 61 61 61 61 61 6	3942	90	245	548	513	543	1621	1819	338	447	555	311	362	397	416	439
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0 1 1 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	61	9	9	9	59.5	59.5	59.5	59.5	29	59	29	58.5	58.5	58.5	58.5	58.5
	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

```
Nypothetical protein C36E8.3 - Caenorhabditis elegans
                                          C;Species: Caenorhabditis elegans
```

C; Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004

C;Accession: T19786 R;Wilkinson, J.; Barlow, K. submit-to the EMB. Data Library, August 1994 A;Reference number: Z19177

A; Accession: T19786

A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA A; Residues: 1-476 <WIL>

A;cross-references: UNIPROT:018500; EMBL:235597; PIDN:CAA84646.1; GSPDB:GN00021; CESP:C3 A;Experimental source: clone C36E8 C; Genetics:

A;Map position: 3 A;Introns: 23/1; 101/3; 152/3; 206/3; 235/1; 255/3; 320/1; 445/2 C;Superfamily: Caenorhabditis elegans hypothetical protein C36E8.3 A; Gene: CESP: C36E8.3

Gaps 8 37.0%; Score 137; DB 2; Length 476; 37.0%; Pred. No. 8.4e-08; tive 11; Mismatches 27; Indels Query Match
Best Local Similarity 37.08
Matches 27; Conservative

23 1 YHRIELDPSKVTSMSAVEFTPLPTCLQHRSCDACMSSDLT-FNCSWCHVLQR----CSg Š

357 ВАĞLHRRRÖНЖFЕ 369 54 -SGFDRYRQEWMD 65 . 유 ò

semaphorin receptor VESPR - human

C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004
C;Accession: T09074
R;Comeau, M.R.; Johnson, R.; DuBose, R.F.; Petersen, M.; Gearing, P.; van den Bos, T.; P
R;Comeau, M.R.; Johnson, R.; DuBose, R.F.; Petersen, M.; Gearing, P.; van den Bos, T.; P
A;Title: A poxvirus-encoded semaphorin induces cytokine production from monocytes and bi
A;Reference number: 216555; MUID:98246049; PMID:9586637

A; Accession: T09074

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Cross-references: UNIPROT:060486; EMBL:AF030339; NID:g3176761; PIDN:AAC18823.1; PID:g3
A;Experimental source: tissue type foreskin; cell type fibroblast

A; Gene: VESPR

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A Residues: 1-1884 «KAM»

A Residues: 1-1884 «KAM»

A Cross-references: UNIPOT:P70207; DDBJ:D86949; NID:g1655431; PIDN:BAA13189.1; PID:d101

C; Comment: This protein is a membrane protein with cell adhesion properties.

C; Keywords: duplication; transmembrane protein

F; 1-21/Domain: signal sequence #status predicted «SIG»

F; 501-549 Region: cysteine-rich duplication

F; 646-691/Region: cysteine-rich duplication

F; 794-845/Region: cysteine-rich duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Accession: T13937
R;Winberg, M.L.; Noordermeer, J.N.; Tamagnone, L.; Comoglio, P.M.; Spriggs, M.K.; Tessie Eell 95, 903-916, 1998
A;Title: Plexin A is a neuronal semaphorin receptor that controls axon guidance. A;Reference number: Z17621; MUID:99091049; PMID:9875845
A;Accession: T13937
                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-1905 <OHT>
A;Cross-references: UNIPROT:Q91823; GB:D38175; NID:g961514; PIDN:BAA07374.1; PID:g961515
C;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: UNIPROT:096681; EMBL:AF106932; NID:94056673; PID:9405674; PIDN:AAD0
                                                                                                                                                                           Riohta, K.; Mizutani, A.; Kawakami, A.; Murakami, Y.; Kasuya, Y.; Takagi, S.; Tanaka, H. Weuron 14, 1189-1199, 1995
A;Title: Plexin: a novel neuronal cell surface molecule that mediates cell adhesion via A;Reference number: I51553; MUID:95329274; PMID:7605632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S.; Hirata, T.; Fujisawa,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7
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C;Species: Drosophila melanogaster
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
                                                Plexin - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plexin 2 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1905;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        486 DRQYIYAMTEKQVTRVPVESCEQYESCDTCLGS-RDPHCGWCVLHNMCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 1884;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 DPSKVTSMSAVEFT--PLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: JC4975
R; Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, Biochem. Biophys. Res. Commun. 226, 396-402, 1996
A; Title: Identification of plexin family molecules in mice. A; Reference number: JC4975; MUID:96400270; PMID:8806646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;794-845/Region: cysteine-rich duplication
F;1223-1250/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
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                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 20.5%; Score 76; DB 2
Best Local Similarity 32.1%; Pred. No. 2;
Matches 17; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.7%; Score 76.5; DE 32.7%; Pred. No. 1.8; tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: JC4975
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 32.78
Matches 16; Conservative
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                                                                                                                                                    C;Accession: ]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein KO4B12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: T21999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21298
R;Steward, C.
Submitted to the EMBL Data Library, December 1996
A;Reference number: Z19723
A;Accession: T22398
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1806 <WILL>
A;Cross-references: UNIPROT: O45657; EMBL: Z83232; PIDN: CAB05755.1; GSPDB: GN00020; CESP: KG
A;Experimental source: clone K04B12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Molecule type: mRNA
**Residues: 1-1872 - KRNA
**Residues: 1-1872 - KRNA
**Residues: 1-1872 - KRNA
**A; Reconses: 1-1872 - KRNA
**A; Cross-references: UNINPROT: P70208; DDBJ: D86950; NID: 91655433; PIDN: BAA13190.1; PID: d101
C; Comment: This protein is a membrane protein with cell adhesion properties.
C; Comment: This protein is a membrane protein
F; H-19/Domain: signal sequence #status predicted <SIG>
F; 1-19/Domain: signal sequenchrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: CESP:K04B12.1
A;Map position: 2
A;Introns: 24/2; 77/3; 294/2; 378/3; 433/3; 478/3; 523/3; 743/1; 794/3; 1049/3; 1414/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plexin 3 precursor - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 09-Jul-2004
C;Accession: JC4976
R;Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, Biochem. Biophys. Res. Commun. 226, 396-402, 1996
A;Title: Identification of plaxin family molecules in mice.
A;Reference number: JC4975; MUID:96400270; PMID:8806646
A;Status: nucleic acid sequence not shown
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                                                                                                                          Gaps
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Pred. No. 1.4;
5; Mismatches 18; Indels 1
                                                      27.3%; Score 101; DB 2; Length 1568; 29.7%; Pred. No. 0.0027; ive 15; Mismatches 27; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 22.7%; Score 84; DB 2; Length 1806; 1 Similarity 43.3%; Pred. No. 0.24; 13; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 SEKQVSQLPVETČEQYLSCAACLGSG-DPHCGWCVLQHRC 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRC
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C; Keywords: receptor; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
20.9%;
Best Local Similarity 40.0%;
Matches 16; Conservative
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                                                                                                                       Conservative
                                                                                       Similarity
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                                                             Query Match
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A; Title: The Met receptor tyrosine kinase transduces motility, proliferation, and morpho A; Reference number: A45453; MUID:93209981; PMID:8384622
                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: hepatocyte growth factor receptor; protein kinase homology
C;Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;
C;1-24/Domain: signal sequence #status predicted <5G5-
F;25-929/Domain: extracellular #status predicted <5K7-
F;25-930/Pomain: extracellular #status predicted <5K7-
F;25-302/Product: hepatocyte growth factor receptor alpha chain #status predicted <ACH->F;308-1379/Product: hepatocyte growth factor receptor beta chain #status predicted <8CH->F;308-1379/Domain: transmembrane #status predicted <TMM->F;955-1379/Domain: intracellular #status predicted <INT->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A;Ro06; MIDI:99069613; PMID:9816316.
A;Note: see websites genome.wustl.edu.gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1108/Active site: Lys #status predicted F;1233/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation) #status predict
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K;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable flavonol 3-O-glucosyltransferase [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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A;Note: the authors translated the codon ACG for residue 1261 as Lys R;Weidner, K.M.; Sachs, M.; Birchmeier, W.
J. Cell Biol. 121, 145-154, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18 EFTPLPT----CLOHRSCDACMSSDLTFNCSWCH----VLORCSSG 55
                                                                                                                                                                                                            A;Status: preliminary; not compared with conceptual translation
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R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998
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Pred. No. 7.2;
5; Mismatches
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Best Local Similarity 30.4%;
Matches 14; Conservative
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A; Residues: 924-935 < WEI>
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A;Regidues: 1-465 <STO>
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A;Residues: 1-1894 «KAM»
A;Cross-references: UNIPROT:P70206; DDBJ:D86948; NID:g1665756; PIDN:BAA13188.1; PID:d101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Experimental source: brain
C, Comment: This protein is a membrane protein, and plays a role in reuronal cell contact
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N;Contains: protein-tyrosine kinase (EC 2.7.1.112) met
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S01254; JH0115; Ā45453
C;Accession: Mu.L.; King, H.W.S.; Deakin, E.A.; Tempest, P.R.; Hilkens, J.; Kroezen, V.; Edw
Oncogene 2, 593-599, 1988
A;Title: Characterization of the mouse met proto-oncogene.
A;Reference number: S01254; MUID:88262253; PMID:2838789
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A; Residues: 1-1379 < CHA>
A; Residues: 1-1379 < CHA>
A; Cross-references: UNIPROT: P16056; EMBL: Y00671; NID: 953058; PIDN: CAA68680.1; PID: 953059
R; Wilks, A.F.; Kurban, R.R.; Hovens, C.M.; Ralph, S.J.
Gene 85, 67-74, 1989
A; Title: The application of the polymerase chain reaction to cloning members of the prot
A; Reference number: JH0112; MUID: 90152381; PMID: 2482828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CjAccession: JC4980
R;Kameyama, T.; Murakami, Y.; Suto, F.; Kawakami, A.; Takagi, S.; Hirata, T.; Fujisawa, Biochem. Biophys. Res. Commun. 226, 524-529, 1996
A;Title: Identification of a neuronal cell surface molecule, plexin, in mice. A;Reference number: JC4980; MUID:96400291; PMID:8806667
A;Accession: JC4980
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C;Species: Mus musculus (house mouse)
C;Date: 31-Dec_1996 #sequence_revision 31-Dec-1996 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                    Length 1945;
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                                                                                                                                                                    A;Description: may function as repellents during axon guidance C;Keywords: cell adhesion; nerve
                                                                                                                                                                                                                                                                                                                                                        11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; Indels
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A;Residues: 'I',1200-1254,'R',1256-1260,'T',1262-1268 <WIL>
A;Experimental source: hemopoietic cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sence of calcium ions.
C;Keywords: duplication; transmembrane protein
C;1.22/Domain: signal sequence #status predicted <SIG>P;1.22/Domain: signal sequence #status predicted <SIG>P;1.238-1264/Domain: transmembrane #status predicted <TMM>P;1238-1264/Domain: transmembrane #status predicted <TMM>P;1266-1268/Region: hydrophilic
                                                                                                                                                                                                                                                                            Score 75; DB:
Pred. No. 2.7;
3; Mismatches
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812 QSCGLCLKADPRFECGWCVAERRCS 836
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                                       A;Gene: plexA
A;Cross-references: FlyBase:FBgn0025741
                                                                                                                                                                                                                                                                                20.3%;
                                                                                                                                                                                                                                                                     Query Match 20.3
Best Local Similarity 44.8
Matches 13; Conservative
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                                                                                                        A, Map position: 4
C, Function:
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A,Title: Identification of the major autophosphorylation site of the Met/hepatocyte grown A;Reference number: A40179; MUID:92011756; PMID:1655790
A;Contents: annotation; autophosphorylation site
R;Dean, M.; Park, M.; Vande Woude, G.F.
Mol. Cell. Biol. 7, 921-924, 1987
A;Title: Characterization of the rearranged tpr-met oncogene breakpoint.
A;Reference number: 157632; MUID:87144265; PMID:3821733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A map position: 7431-7431
C; Superfamily: hepatocyte growth factor receptor; protein kinase homology
C; Superfamily: hepatocyte growth factor receptor; protein; phosphoprotein; phosphotransferase; ]
C; Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase; ]
C; L4, Domain: signal sequence #status predicted <100.
F; 130-1390/Product: hepatocyte growth factor receptor alpha chain #status predicted <ALP-F; 3108-1390/Product: hepatocyte growth factor receptor beta chain #status predicted <ALP-F; 101-1344/Domain: protein kinase homology <KIN-F; 101-1344/Domain: protein kinase ATP-binding motif F; 1014-1092/Region: protein kinase ATP-binding site: carbohydrate (Asn) (covalent) #status F; 1110/Active site: Lys #status experimental F; 1110/Active site: phosphate (Tyr) (covalent) (by autophosphorylation) #status experimental F; 1215/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           plasminogen related growth factor receptor 2 - Fugu rubripes
C;Species: Rugu rubripes
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
C;Accession: T30813
R;Cottage, A.J.; Clark, M.; Hawker, K.; Umrania, Y.; Wheller, D.; Bishop, M.; Elgar, G.
PRES Lett. 443, 370-374, 1999
A;Title: Three receptor genes for plasminogen related growth factors in the genome of the A;Reference number: 220880; MUID:99148833; PMID:10025966
                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M15325; NID:g187531; PIDN:AAA59585.1; PID:g187532
C;Comment: The receptor is a dimer of disulfide-bonded 50K alpha and 145K beta chains th.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:Q9YGM5; EMBL:AJ010348; NID:e1355080; PID:e1355082; PIDN:CAA0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Introns: 400/3; 459/3; 499/3; 556/3; 611/2; 655/3; 701/2; 761/2; 794/3; 870/3; 919/3; C;Superfamily: hepatocyte growth factor receptor; protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.4%; Score 68; DB 1; Length 1390; 30.4%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 EFTPLPT----CLQHRSCDACMSSDLTFNCSWCH----VLQRCSSG 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 KVTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWC 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.2%; Score 67.5; DB ilarity 32.4%; Pred. No. 14; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plexin B - fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDB:120178; OMIM:164860
                                                                                                                                                                                                                                                                                                        A;Scatus: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 963-1009 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 30.4 nes 14; Conservative
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les 12; Conserv
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Matches
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A; Residues: 'VNETRECOSLALELEKLANOQLKALTEKNKELEIAQDRNIALQSQ','FTRTKEELEAEKRDLIRTNERLSQELEBY
A; Residues: 'VNETRECOSLALELEKLANOQLKALTEKNKELEIAQDRNIALQSQ','FTRTKEELEAEKRDLIRTNERLSQELEBY
A; Cross=references: GB: U08818; NID: 9487741; PIDN: AAB60323.1; PID: 9487742
A; Note: this activated met oncogene is the product of gene rearrangement
R; Dean, M.; Park, M.; Le Beau, M.M.; Robins, T.S.; Diaz, M.O.; Rowley, J.D.; Blair, D.G.
Nature 318, 385-388, 1985
A; Title: The human met oncogene is related to the tyrosine kinase oncogenes.
A; Reference number: A93369; MUID: 86065462; PMID: 4069211
A; Accession: A93369
A; MOLOCULE type: DNA
A; Residues: 1267-1390 < DEA>
A; Gondano, S.; Comoglio, P.M.; Santoro, C.
J. Biol. Chem. 269, 12852-12857, 1994
A; Reference number: A53761; MUID: 94230365; PMID: 8175700
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A,Rebidues: 1-1390 cs10.>
A,Rebidues: 1-1390 cs10.>
A,Cross-references: UNIPROT: P08581; EMBL:XE4559
R;Park, M.; Dean, M.; Kaul, K.; Braun, M.J.; Gonda, M.A.; Vande Woude, G.
R;Park, M.; Dean, M.; Kaul, K.; Braun, M.J.; Gonda, M.A.; Vande Woude, G.
R;Park, M.; Dean, M.; Kaul, K.; Braun, M.J.; Gonda, M.A.; Vande Woude, G.
A,Title: Sequence of MET protooncogene cDNA has features characteristic of the tyrosine
A,Reference number: A28303; MUID:87317655; PMID:2819873
                                                                                                                                                                                                                                     A,Cross-references: UNIPROT:Q9ZU71; GB:AE002093; NID:g4218003; PIDN:AAD12211.1; GSPDB:GN
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A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A,Reference number: A84420; MUID:20083487; PMID:10617197
A,Accession: G84565
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-444 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatocyte growth factor receptor precursor - human N;Contains: protein-tyrosine kinase (EC 2.7.1.112) met C;Species: Homo sapiens (man) 30-Sepecies: Homo sapiens (man) C;Date: 31-Mar-1991 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004 C;Accession: A40175; A28303; A93369; A53761; I57632; A30008; B24569 R;Giordano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A;Residues: 1-755, 'TWWKEPLNIVSFLFCFAS', 756-1190,'A',1192-1390 <PAR>
A;Residues: 1-755, 'TWWKEPLNIVSFLFCFAS', 756-1190,'A',1192-1390 <PAR>
A;Crose-references: GB:002988; NID:918758; PIDN:AAA55591.1; PID:9307196
R;Chan, A.M.L.; King, H.W.S.; Tempest, P.R.; Deakin, E.A.; Cooper, C.S.; J
Oncogene 1, 229-233, 1987
Oncogene 1, 229-233, 1987
A;Title: Primary structure of the met protein tyrosine kinase domain.
A;Reference number: A93749; MUID:88143699; PMID:3325883
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A,Residues: 1-14 <62AM>
R.Ferracini, R.; Longati, P.; Naldini, L.; Vigna, E.; Comoglio, P.M.
R.Ferracini, Chem. 266, 19558-19564, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 69; DB;
; Pred. No. 3.4;
13; Mismatches
                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: At2g18560
A;Map position: 2
C;Superfamily: flavonol O3-glucosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 24.6%;
Matches 16; Conservative 1:
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EQWMN 362
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C; Accession: T13164

B; Winberg, M.L.; Noordermeer, J.N.; Tamagnone, L.; Comoglio, P.M.; Spriggs, M.K.; Tessie Cell 95, 903-916, 1998
A; Title: Plaxin A is a neuronal semaphorin receptor that controls axon guidance.
A; Reference number: Z17621; MUID: 99091049; PMID: 9875845
A; Accession: T13164
A; Accession: T13164
A; Accession: T13164
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-2051 aWINA
A; Residues: 1-2051 aWINA
A; Cross=references: UNIPROT: 096682; EMBL: AF106933; NID: 94056675; PID: 94056676; PIDN: AADG C; Genetics:
A; Gene: plexB
A; Cross=references: FlyBase: FBgn0025740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: plays a role in neuronal cell contact, axon guidance and fasciculation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 67.5; DB 2; Length 2051;
Pred. No. 19;
9; Mismatches 23; Indels 5;
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Best Local Similarity 28.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position: 4
C; Function:
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S13 MSPKKDFLYVLSQRKITKLRIEHCSVYTNCSACLESRDPF-CGWCSLEKRCT 563 6 LDPSK----VTSMSAVEFTPLPTCLQHRSCDACMSSDLTFNCSWCHVLQRCS 53 ઠ

RESULT 15
813149
periplasmic nitrate reductase small chain (cytochrome C-type protein) Cj0783 [imported]
C;Species: Campylobacter jejuni
C;Species: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 09-Jul-2004 g

C;Accession: G81349
R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chillin C.W.; Quall, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Barrel Nature 403, 655-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp. A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Status: preliminary

A;Molecule type: DNA \*Residues: 1-174 «PAR» A;Cross-references: UNIPROT:Q9PPD6; GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB7304 A;Experimental source: serotype O2, strain NCTC 11168

C;Genetics: A;Gene: napB; Cj0783 C;Superfamily: cytochrome c-type protein napB

Gaps 4; Score 67; DB 2; Length 174; Pred. No. 2.5; 2; Mismatches 14; Indels ch 18.1%; .1 Similarity 42.9%; 15; Conservative Matches

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ઠે 셤 Search completed: January 28, 2005, 22:12:42 Job time : 7.50139 secs

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Sequence 3712, Ap
                                                                                                                                      January 28, 2005, 21:59:20 ; Search time 29.518 Seconds (without alignments) 1321.880 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB_pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_PUB_COMB.pep:*

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6: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB_pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

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10: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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588
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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score greater than or equal to
and is derived by analysis of
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seq length: 200000000
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Match Length
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Perfect score:
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Maximum DB
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64 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVABLMANFNBGYSDNSTVVYFD 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 240;
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APPLICANT CONTACTORY

TITLE OF INVENTION: NO. US20030236392Alel full length cDNA FILER REFERENCE: H1-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096

SOFTWARE: APPLICATION VET: 2.1

ERGO ID NO 3712

LENGTH: 240
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100.0%; Score 588; DB 14;
Best Local Similarity 100.0%; Pred. No. 1.4e-60;
Matches 108; Conservative 0; Mismatches 0;
US-10-156-487A-6
US-10-474-794-192
US-10-474-794-192
US-09-912-935-23
US-09-912-935-23
US-09-912-935-35
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US-09-912-935-40
US-09-912-935-40
US-10-176-758-472
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US-10-176-758-472
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Publication No. US20030236392A1
GENERAL INFORMATION:
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US-09-912-935-36
; Sequence 36, Application US/09912935
  tryPE: PRT
CORGANISM: Homo sapiens
US-10-104-047-3712
 US-10-104-047-3712
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Sequence 230, Appl Sequence 230, Appl Sequence 2, Appli Sequence 5, Appli Sequence 179, Appl Sequence 179, Appl Sequence 192, Appl Sequence 297, Appl

Sequence 36, Appl Sequence 36, Appl Sequence 4, Appli

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APPLICANT: Alvarez, Enrique
APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
Publication No. US20040259774A1
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Best Local Similarity
                        GENERAL INFORMATION
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US-09-918-715-230
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SEQ ID NO 4
LENGTH: 488
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APPLICANT:
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                   GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT PILING DATE: 2001-07-24
PRIOR RELING DATE: 2000-12-23
NUMBER: OF SEQ ID NOS: 53
SOFTWARE: PALENTIN Version 3.0
SEQ ID NO 36
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APPLICANT: Labat, Ivan
APPLICANT: Labat, Ivan
APPLICANT: Liu, Chenghua
APPLICANT: Chids, John
APPLICANT: Chao, Cheng-Chi
APPLICANT: Chao, Cheng-Chi
APPLICANT: Dramand, Radoje T
APPLICANT: Lee, Juhi
ITILE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFRENCE: 30266/37630
CURRENT APPLICATION NUMBER: US/10/168,365
CURRENT APPLICATION NUMBER: US/10/168,365
CURRENT PILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 36
SOFTMARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
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100.0%; Pred. No. 2.9e-60;
ive 0; Mismatches 0; Indels 0
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100.0%; Pred. No. 2.9e-60;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 36, Application US/10168365; Publication No. US20030211987A1; GENERAL INFORMATION:
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US-10-357-819-4
; Sequence 4, Application US/10357819
  US20030022825A1
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Matches 108; Conservative
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Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-168-365-36
  Publication No.
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US-10-168-365-36
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LENGTH: 431
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APPLICANT; Zhong, Me.

APPLICANT; Zhong, Me.

FILE REFERENCE: 21402-538A

CURRENT APPLICATION NUMBER: US/10/357,819

CURRENT APPLICATION NUMBER: 09/520,781

PRIOR APPLICATION NUMBER: 09/520,781

PRIOR FILING DATE: 2000-03-08

PRIOR FILING DATE: 2000-03-14

PRIOR FILING DATE: 2000-05-31

PRIOR PILING DATE: 2000-05-31

PRIOR PILING DATE: 2000-02-14

PRIOR PILING DATE: 2002-02-14

PRIOR APPLICATION NUMBER: 09/783,436

PRIOR PILING DATE: 2002-02-5

PRIOR APPLICATION NUMBER: 60/353,301

PRIOR PILING DATE: 2002-02-01

PRIOR PILING DATE: 2002-02-01

PRIOR PILING DATE: 2002-02-01

PRIOR PILING DATE: 2002-02-12

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PRIOR PILING DATE: 2002-02-12

PRIOR APPLICATION NUMBER: 60/358,608

PRIOR PILING DATE: 2002-02-12

PRIOR APPLICATION NUMBER: 60/358,608

PRIOR PILING DATE: 2002-02-12

PRIOR APPLICATION NUMBER: 60/358,367

PRIOR PILING DATE: 2002-02-12

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SEQ ID NOS: 142
CuraSeqList version 0.1
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                                                                                                                                                                                                                                     Padigaru, Muralidhara
                                                                                                                                                                                                                                                                                                                                                                                                           Shenoy, Suresh G.
Shimkets, Richard A.
Spytek, Kimberly A.
                                                                                                                                        Li, Li
Miller, Charles E.
                                                                                                                                                                                                                                                                            Patturajan, Meera
Rastelli, Luca
                                                                                                                                                                                                                                                                                                                                                                              Rieger, Daniel K.
Guo, Xiaojia
Ji, Weizhen
Kekuda, Ramesh
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD PILE REPERENCE: 21402-538A CURRENT APPLICATION NUMBER: US/10/357,819 CURRENT FILING DATE: 2003-02-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 196
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                                                             APPLICANT: Carson-Walter, Bleanor
APPLICANT: Carson-Walter, Bleanor
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR PILING DATE: 2001-04-11
PRIOR PILING DATE: 2001-04-11
PRIOR FILING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: BASESEQ for Windows Version 4.0
SEQ ID NO 230
LENGTH: 500
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; Pred. No. 3.5e-60;
0; Mismatches 0;
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PRIOR FILING DATE: 2000-03-08
PRIOR PLING DATE: 2000-03-08
PRIOR PLING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/783,436
PRIOR APPLICATION NUMBER: 09/783,436
PRIOR APPLICATION NUMBER: 10/085,198
PRIOR FILING DATE: 2002-02-25
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FILING DATE: 2002-02-01
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APPLICATION NUMBER: 60/355,099
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Spytek, Kimberly A.
Zhong, Mei
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APPLICANT: Edinger, Shlomit R.
APPLICANT: Gangolli, Esha A.
APPLICANT: Gerlach, Valerie L.
APPLICANT: Gorman, Linda
Publication No. US20040213793A1
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Miller, Charles E.
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Shenoy, Suresh G.
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Best Local Similarity 100.0
Matches 108; Conservative
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Kekuda, Ramesh
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US-10-474-794-230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
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                          TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/22,599
PRIOR PILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: 60/224,360
PRIOR PILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SOUTHARE: PSELSEQ for Windows Version 3.0
SEQ ID NO 230
LENGTH: 500
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; Pred. No. 3.5e-60;
0; Mismatches 0;
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US-10-474-794-230
; Sequence 230, Application US/10474794
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100.0%;
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    Kenneth Kinzler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 108; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , ORGANISM: Homo sapiens
US-09-918-715-230
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ORGANISM: Homo sapiens
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Best Local (
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        APPLICANT:
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Sequence 5, Application US/10156487A

Publication No. US20030092025A1

GENERAL INFORMATION:

APPLICANT: Juan, Todd

APPLICANT: Oliner, John

TILLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof

TILLE OF INVENTION: Tumor Endothelial Marker 7a Molecules and Uses Thereof

CURRENT FILING DATE: 2002-09-10

PRIOR APPLICATION NUMBER: US/10/156,487A

CURRENT APPLICATION NUMBER: 60/293,852

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 502
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PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: 60/356,424
PRIOR PILING DATE: 2002-02-12
PRIOR PILING DATE: 2002-02-12
PRIOR PLICATION NUMBER: 60/358,239
PRIOR PLICATION NUMBER: 60/358,608
PRIOR PILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-25
PRIOR PLING DATE: 2002-02-25
PRIOR PRIOR APPLICATION NUMBER: 60/359,367
PRIOR PLING DATE: 2002-02-25
NUMBER OF SEQ ID NOS: 142
SOFTWARE: CuraSeqList version 0.1
SOFTWARE: CuraSeqList version 0.1
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                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CRGANISM: Homo sapiens
US-10-357-819-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
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US-09-918-715-179
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US-10-156-487A-5
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Sequence 179, Application US/09918715; Publication No. US20030017157A1; GENERAL INFORMATION: APPLICANT: Brad St. Croix; APPLICANT: Bert Vogelstein

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137 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 196
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100.0%; Score 588; DB 10; Length 1002;
Best Local Similarity 100.0%; Pred. No. 8.4e-60;
Matches 108; Conservative 0; Mismatches 0; Indels 0;
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Sequence 179, Application US/10474794

Publication No. US20040213793A1

GENERAL INFORMATION:

APPLICANT: Carson-Walter, Eleanor

APPLICANT: St. Croix, Brad

APPLICANT: Kinzler, Kenneth

TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS

FILE REFRENCE: 1107.00179

CURRENT APPLICATION NUMBER: US/10/474,794

CURRENT APPLICATION NUMBER: 60/282,850

PRIOR APPLICATION NUMBER: 60/282,850

PRIOR APPLICATION NUMBER: 60/282,850

PRIOR FILING DATE: 2001-04-11

PRIOR FILING DATE: 2001-04-11

PRIOR FILING DATE: 2001-08-01

NUMBER OF SEQ ID NOS: 359

SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Kenneth Kinzler
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT PEPLICATION NUMBER: 0/202,599
PRIOR APPLICATION NUMBER: 60/222,599
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-02
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
SPIOR POPLICATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR PILING DATE: 2000-08-11
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100.0%; Pred. No. 8.4e-60;
ive 0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 108; Conservative C
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US-10-474-794-179
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US-10-474-794-179
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US-09-918-715-192
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Publication No. US20030017157A1

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ORGANISM: Mus musculus
US-10-474-794-192
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Pred. No. 3.9e-53;
4; Mismatches 5; Indels
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Sequence 297
Sequence 297
Sequence 297
Publication No. US20030017157A1
GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Brad St. Croix
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 06/22,599
PRIOR PPLICATION NUMBER: 60/22,599
PRIOR PPLICATION NUMBER: 60/22,599
PRIOR PLILING DATE: 2000-08-02
PRIOR PLILING DATE: 2000-08-01
PRIOR PLILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
PRIOR FILING DATE: 2000-04-11
SAQ ID NO.297
LENGTH: 500
SEQ ID NO.297
LENGTH: 500
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GENERAL INFORMATION:
APPLICANT: Brad St. Croix
APPLICANT: Bert Voglatein
APPLICANT: Bert Voglatein
APPLICANT: Rent Voglatein
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00134
CURRENT APPLICATION NUMBER: US/09/918,715
CURRENT FILING DATE: 2001-08-01
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 2000-08-11
STOR RELIGATION NUMBER: 60/282,850
PRIOR FILING DATE: 2000-04-11
NUMBER OF SEQ ID NOS: 358
SEQ ID NO 192
LENGTH: 500
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Pred. No. 3.9e-53;
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Best Local Similarity 91.5%;
Matches 97; Conservative
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Best Local Similarity 91.5%;
Matches 97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Mus musculus
US-09-918-715-192
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US-09-918-715-297
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198 NGTVFVVQWDHVYLQDREDRGSFTFQAALHRDGRIVFGYKEIPMAV 243

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APPLICANT: Juan, Tood
APPLICANT: Dass, Michael B.
APPLICANT: Bass, Michael B.
APPLICANT: Oliner: John
TITLE OF INVENION: Tumor Endothelial Marker 7a Molecules and Uses Thereof
FILE REFERENCE: 01-072-A
CURRENT APPLICATION WUMBER: US/10/156,487A
CURRENT FILING DATE: 2002-09-10
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
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Pred. No. 3.9e-53;
4; Mismatches 5; Indels (
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APPLICANT: Carson-Walter, Bleanor
APPLICANT: St. Croix, Brad
APPLICANT: St. Croix, Brad
APPLICANT: Vogelstein, Bert
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: ENDOTHELIAL CELL EXPRESSION PATTERNS
FILE REFERENCE: 1107.00179
CURRENT APPLICATION NUMBER: US/10/474,794
CURRENT FILING DATE: 2003-10-14
PRIOR APPLICATION NUMBER: 60/282,850
PRIOR PELING DATE: 2001-04-11
PRIOR PELING DATE: 2001-04-11
PRIOR PELING DATE: 2001-08-01
NUMBER OF SEQ ID NOS: 359
SOFTWARE: FASTSEQ for Windows Version 4.0
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Pred, No. 3.9e-53;
4; Mismatches 5;
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Publication No. US20040213793A1
GENERAL INFORMATION:
Sequence 6, Application US/10156487A Publication No. US20030092025A1 GENERAL INFORMATION:
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91.5%;
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Best Local Similarity 91.5%;
Matches 97; Conservative
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Best Local Similarity 91.55
Matches 97; Conservative
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Search completed: January 28, 2005, 22:19:18 Job time : 33.518 secs

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LENGTH: 431
TYPE: PRT
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Sequence 25, Appl
Sequence 34, Appl
Sequence 31, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 2, Appl
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Sequence 1, Appli
Sequence 1995, Appli
Sequence 16, Appli
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                                                                                                  January 28, 2005, 21:56:43 ; Search time 8.77562 Seconds
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(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Compugen Ltd.
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US-09-764-325A-23

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US-09-912-935-35

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US-09-912-935-34

US-09-912-935-38

US-08-746-797-2

US-08-746-797-2

US-08-746-797-2

US-08-746-797-2

US-08-918-088-1

US-09-543-61A-4675

US-09-543-66A-4

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APPLICATION MICHAEL AND MITSUO ET Al.
TITLE OF INVENTION: METHORS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFFWARE: Patentin version 3.0
SEQ ID NO 36
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US-09-764-325A-23
is Application US/09764325A
j Patent No. 6667391
j GENERAL INFORMATION:
j APPLICANT: Labat, Ivan
j APPLICANT: Tama, Y. T.
j APPLICANT: Tama, Y. T.
j APPLICANT: Mize, Nancy K.
j APPLICANT: Chao, Cheng-Chi
j APPLICANT: Chao, Cheng-Chi
j APPLICANT: Mize, Nancy K.
j APPLICANT: Mize, Nancy K.
j TILLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell
j TILLE OF INVENTION: Growth Factor-Like Polypeptides and Polynucleotides
j TILLE REFERENCE: 30266/37630A
j CURRENT APPLICATION NUMBER: US/09/764,325A
j CURRENT FILING DATE: 2001-01-16
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100.0%; Pred. No. 2e-66;
ative 0; Mismatches 0; Indels
                                                                              US-09-195-666A-49
US-09-309-592-6
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US-09-634-858A-5
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US-09-257-525A-9
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US-09-11-540-6
US-09-329-922B-2
US-09-342-394-2
US-09-118-709-2
US-09-118-709-2
US-09-118-709-2
US-09-118-709-2
US-09-118-709-2
US-09-583-110-2877
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| JENUICANT: Labat, Ivan
| APPLICANT: Labat, Ivan
| APPLICANT: Labat, V. T. |
| APPLICANT: Tang, Y. T. |
| APPLICANT: Tang, Y. T. |
| APPLICANT: Chao, Cheng-Chi |
| APPLICANT: Chao, Cheng-Chi |
| APPLICANT: Childs, John |
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell |
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell |
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell |
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell |
| TITLE OF INVENTION: Methods and Materials Relating to No. 6667391el Stem Cell |
| TITLE OF INVENTION NUMBER: 09/547,358 |
| PRIOR FILING DATE: 2000-04-01 |
| PRIOR PELING DATE: 2000-04-07 |
| PRIOR APPLICATION NUMBER: 09/545,714 |
| PRIOR APPLICATION NUMBER: 09/545,714 |
| PRIOR PELING DATE: 2000-04-07 |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 70.9%; Score 417; DB 4; Length 392; Best Local Similarity 72.2%; Pred. No. 1.1e-44; Matches 78; Conservative 12; Mismatches 18; Indels
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PRIOR APPLICATION NUMBER: Us/s4/,550
PRIOR FILING DATE: 2000-04-11
PRIOR PLING DATE: 2000-04-07
PRIOR RILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 23
LENGTH: 392
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US-09-912-935-23
; Sequence 23, Application US/09912935
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 25, Application US/09912935

Sequence 25, Application US/09912935

Sequence 25, Application US/09912935

Sequence 25, Application US/09912935

GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT PILING DATE: 2001-07-24

PRIOR FILING DATE: 2000-12-23

NUMBER: OF SEQ ID NOS: 53

SOFTWARE:
LENGTH: 392

LENGTH: 392
APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37483
CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR PILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 392
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Patent No. 6673904
GENERAL INFORMATION:
APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
APPLICANT: Nishikawa, Mitsuo et al.
ATITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE;
ITITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 70.9%; Score 417; DB 4; Best Local Similarity 72.2%; Pred. No. 1.1e-44; Matches 78; Conservative 12; Mismatches 18;
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Best Local Similarity 72.2%
Matches 78; Conservative
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US-09-912-935-25
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US-09-912-935-23
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US-09-912-935-35
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Sequence 40, Application US/09912935
Patent No. 6673904
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE
TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES
FILE REFERENCE: 32066/37488
CURRENT APPLICATION NUMBER: US/09/912,935
FILE REPRESENCE: 2001-07-24
FRIOR APPLICATION NUMBER: PCT/US00/35260
FRIOR PILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Nishikawa, Mitsuo et al.

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFERENCE: 32066/37483

CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT APPLICATION NUMBER: PCT/US00/35260

PRIOR FILING DATE: 2001-07-24

PRIOR FILING DATE: 2000-12-23

NUMBER: OF SEQ ID NOS: 53

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 28
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; Pred. No. 1.5e-44;
12; Mismatches 18;
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Patent No. 6673904
NUMBER OF SEQ ID NOS: 53
SOFTWARE: PatentIn version 3.0
SEQ ID NO 31
LENCTH: 499
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                                                                                                                                                                                                                                                   78; Conservative
                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
US-09-912-935-31
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US-09-912-935-28
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Best Local Similarity
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LENGTH: 529
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Patent No. 6673904

GENERAL INFORMATION:

APPLICANT: NISHIKAWA, MITBUO et al.

TITLE OF INVENTION: METHODS AND MATRIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE

TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFERENCE: 32066/37483

CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT FILING DATE: 2010-07-24

PRIOR FILING DATE: 2010-07-24

NUMBER OF SEQ ID NOS: 53

SOFTWARE: Patentin version 3.0

SEQ ID NO 3.53
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Patent No. 6673904

GENERAL INFORMATION:
FRIED OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE

TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

FILE REFERENCE: 32066/37483

CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT FILING DATE: 2010-07-24

PRIOR FILING DATE: 2000-12-23

PRIOR FILING DATE: 2000-12-23
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                                                                                                                                                                                                                                                                                                                         70.9%; Score 417; DB 4; Length 425; 72.2%; Pred. No. 1.2e-44; ive 12; Mismatches 18; Indels
               CURRENT APPLICATION NUMBER: US/09/912,935
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: PCT/US00/35260
PRIOR FILING DATE: 2000-12-23
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin version 3.0
SEQ ID NO 35
LENGTH: 425
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Best Local Similarity 72.2%
Matches 78; Conservative
  FILE REFERENCE: 32066/37483
                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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US-09-912-935-34
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15 ITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPG------YSDNSTVVYFDN 61
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                                                         CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION UNUBER: No. 5759832 Yet Assigned
FILING DATE: 23-OCT-1996
ATTORNEY/APENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
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ADDRESSEE: SmithKilne Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITI:
STATE: PA
COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READALE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/927,387
"T.ING DATE: 25-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.6%; Score 68; 23.5%; Pred. No.
                 APPLICATION NUMBER: US/08/746,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08927387;
Patent No. 5783432;
GENERAL INFORMATION:
APPLICANT: Gentry, Daniel
APPLICANT: Payne, David
APPLICANT: Payne, David
APPLICANT: Pearson, Stewart
TITLE OF INVENTION: NOVEL FabH
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
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Best Local Similarity 23.5%
Matches 31; Conservative
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220 FAIRDVAKSIKQ 231
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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                          TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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US-08-927-387-2
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Sequence 38, Application US/09912935

Sequence 38, Application US/09912935

Sequence 38, Application US/09912935

Sequence 38, Application US/0904

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO STEM CELL GROWTH FACTOR-LIKE TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES

CURRENT APPLICATION NUMBER: US/09/912,935

CURRENT FILING DATE: 2001-07-24

PRIOR APPLICATION NUMBER: PCT/US00/35260

PRIOR APPLICATION NUMBER: PCT/US00/35260

RECO ID NOS: 53

SOFTWARE: Patentin version 3.0

SEQ ID NO 38

LENGTH: 530
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                                                                Length 529;
                                                                                                        18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08746797; Patent No. 5759832; GENERAL INFORMATION:
APPLICANT: Gentry, Daniel APPLICANT: Lonsdale, John APPLICANT: Payne, David APPLICANT: Pearson, Stewart TITLE OF INVENTION: NOVEL FabH NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: SmithKine Beecham Corporation STREET: 709 Swedeland Road CITY: Ring of Prussia
                                                           70.9%; Score 417; DB 4; 72.2%; Pred. No. 1.6e-44; iive 12; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                                                           Query Match
Best Local Similarity 72.29
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 70.4
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
; ORGANISM: Homo sapiens
US-09-912-935-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: PA
                                                                                                                                                                                                                                                                                                                                                            US-09-912-935-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: SmithKline Beecham Corporation
I: 709 Swedeland Road
King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15 ITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPG
                                                                                                                                                                                                                                                                                                                                                                                                                                    11.6%; Score 68; DB 1
23.5%; Pred. No. 2.6;
tive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 GTVFVV----QWDHVYLQGWEDKGS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 19406-0939
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
SOFTWARE: FastSEQ Version 1.5
TULNG DATE: 25-AUG-1997
CLASSIPICATION AA35
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/746,797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-918-058-2

Sequence 2, Application US/08918058

Patent No. 5885572

GENERAL INFORMATION:

APPLICANT: Gentry, Daniel

APPLICANT: Payne, David

APPLICANT: Payne, David

APPLICANT: Payne, David

APPLICANT: Payne, David

APPLICANT: Payne, David

APPLICANT: Payne, David

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham CO
APPLICATION NUMBER: 08/746,797
           FILING DATE: 23-OCT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward
REGISTRATION NUMBER: 38,891
REFRENCE/DOCKET NUMBER: P505'
TELECOMMUNICATION INFORMATION:
TELECHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTORNEY/AGENT INFORMATION:
NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                             N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 23.5'
Matches 31; Conservative
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                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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ORIGINAL SOURCE:
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CITY: Ki
STATE: P
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Sequence 7887, Application US/09543681A

Factor 7887, Application US/09543681A

Patent No. 6605709

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,1002-001

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT FILING DATE: 2000-04-05

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 7887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16 TIATGGFIFMGDVIHRMLTATQYVAPL--MANFNPGYSDNSTVVYFDNGTVFVVQ----
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                                                                                                                                                                                                                                                                                                                                                                                                   Length 324;
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11.6%; Score 68; DB 2
Best Local Similarity 23.5%; Pred. No. 2.6;
Matches 31; Conservative 19; Mismatches
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26.5%; Pred. No. 2.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 ---WDH-----VYLQGWEDKGS 82
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
TELEFAX: 610-270-5090
                                                                                                       INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                     ; ANTI-SENSE: NO; PRAGMENT TYPE: N-terminal; ORIGINAL SOURCE: US-08-918-058-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7887
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Best Local Similarity 26.5%
Matches 22; Conservative
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220 FAIRDVAKSIKQ 231
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MOLECULE TYPE: peptide
HYPOTHETICAL: NO
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Aaq88850 homo sapien

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P79838 puntius con
P79850 puntius tet
P79858 rasbora ele
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Q8iuk5 homo sapien
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Aaq62573 xenopus l
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1 LSPDFPFYGHPLRQITIATG........LHHDGRIVFAYKEIPMSVPE 108
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                           GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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Maximum Match 100%
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SHH_PUNTE
SHH_RASEL
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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danio frank
danio frank
danio pulch
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OSDIANA A. Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
A Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
A Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R.,
A Cusuki T., Sato H., Wakamatsu A., Umezawa A., Imabayashi H.,
Pukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y.,
A Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K.,
Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y.,
Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AK127539; BAC87025.1; -
EMBL; AK127539; Plaxin_repeat.
R Interpro; IPRO02165; Plaxin_repeat.
R Fam; PFO1437; PSI; 1.
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AC BAC87025

BAC87025

DY 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE CDNA FLJ45632 fis, clone CHONS2011834, highly similar to Homo sapiens tumor endothelial marker 7 (TEM7).

S Homo sapiens (Human).

C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (Human).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                 P79915 G
Q9yh85 G
Q7h86 G
Q8mmc7 G
Q9wmc7 G
Q79440 E
Q79440 E
Q13235 G
Q13234 G
Q13248 G
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100.0%; Pred. No. 6.8e-54;
ive 0; Mismatches 0; Indels (
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                          351 AA
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                 SHH_TANAL
TECA_CHICK
Q7JNB6
Q9W0Y8
SHH AMBCH
Q7Q440
SHH DANAA
SHH_DANAA
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SHH_DANFR
SHH_DANKE
SHH_DANPU
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Best Local Similarity 100.0
Matches 108; Conservative
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Length 500;

DB 2;

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Query Match
Best Local Similarity 100.
Matches 108; Conservative
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                    Oshima A., Takahashi-Pujii A., Tanase T., Imose N., Takeuchi K., Arita M., Musashino K., Yuuki H., Hara H., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamasu A., Umezawa A., Imabayashi H., Fukuma M., Hata J., Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Randa K., Magatsuma M., Murakawa K., Kanehori K., Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K., Isogai T.; "NEDO human CDNA sequencing project."; Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AK127539; BAC87025.1; -- SEQUENCE 351 AA; 39639 MW; FE03CC9D78E4604A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=21443268; PubMed=11559528;
MEDLINE=21443268; PubMed=11559528;
MEDLINE=21443268; Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-ORT-2001 (TrEMBLrel. 18, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Tumor endothelial marker 7 precursor (Tumor endothelial marker 3
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Vogelstein B.,
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                                                                                                                                                                                           Length 351;
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20407466; PubMed=10947988;
St Croix B., Rago C., Velculescu V., Traverso G.,
Montgomery E., Lal A., Riggins G.J., Lengauer C.,
                                                                                                                                                                                        100.0%; Score 588; DB 2;
100.0%; Pred. No. 6.8e-54;
ive 0; Mismatches 0;
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EMBL; AF378753; AAL11990.1; -.
GO; GO:0001525; P:angiogenesis; NAS.
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InterPro; IPR002165; Plexin_repeat.
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SMART; SM00423; PSI; 1
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01-MAR-2001 (
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Kausner R.D., Colling F.S., Wagner L.H., Derge J.G.,

Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

R. Botheron M., Soares M.B., Bonaldo M.P., Casvant T.L., Scheetz T.E.,

R. Brownstein M.J., Usdin T.B., Toohhyuki S., Carninci P., Prange C.,

R. Brownstein M.J., Widin T.B., Toohhyuki S., Carninci P., Prange C.,

R. Brownstein M.J., Widin T.B., Toohhyuki S., Carninci P., Prange C.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McKernan R.J., Malek J.A., Gunarathe P.H.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

R. Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

R. Pahey J., Helton B., Ketteman M., Maddan A., Kodrigues S., Sanchez A.,

R. Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfeard G.G.,

R. Rizyminski M.I., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

R. Mannes S.J., Marra M.A.,

R. Mennes S.J., Marra M.J.,

R. Mennes S.J., Marra M.A.,

R. Mennes S.J., Marra M.J.,

R. Mennes S.J., Marra M.J.,

R. Mennes S.J., Marra M.J.,

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R. Men
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC036659; AAH36659.1;
Genew; HGNC:20945; PLXDCI.
GO, GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IBA.
GO; GO:0007275; P:development; IBA.
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E 500 AA; 55778 MW; 3FA4F9D98A514ABF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
100.0%; Score 588; DB 2
100.0%; Pred. No. 1e-53;
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InterPro, IPR002165; Plexin_repeat
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SMART; SM00423; PSI: 1
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137 LSFDFPFYGHPLRQITMATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 196
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The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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Arakawa T., Bono H., Carninci P., Pukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
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                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone:2410003107 product:TUMOR ENDOTHELIAL MARKER 7 homolog.
Name=Plxdc1;
                          NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
                                                   NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 244
                                                                                                                                                                                                                                                                                                                                                        Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/61;
MEDLINE=99279253; PubMed=10349636;
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                                                                                                                                                                                                                                         Mus musculus (Mouse)
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Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinaqawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
M. Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshino M.,
M. Muramatsu M., Hayashizaki Y.;
M. Muramatsu M., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AK010361; BABZ6881.1; -.
RO; GO:0016020; Cmembrane; IEA.
GO; GO:0016020; Cmembrane; IEA.
GO; GO:0017375; Picceptor activity; IEA.
RO; GO:00160215; Picceptor activity; IEA.
RO; GO:00160215; Picceptor activity.
RINTERPO; IPR00110; Ig-like.
RINTERPO; IPR00110; Ig-like.
RINTERPO; IPR00110; Ig-like.
RINTERPO; IPR00110; PSI: 1.
REMR; SM0423; PSI: 1.
REMR; SM0423; PSI: 1.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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91.5%; Pred. No. 2.4e-47;
ive 4; Mismatches 5; Indels
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tumor endothelial marker 7.
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MEDIINE=21443268; PubMed=11559528;
Carson-Walter E.B., Watkins D.N., Nanda A., Vogelstein
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14FE25512A319DAF CRC64;
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01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
11-Muor endothelial marker 7 precursor.
Name=Plxdcl; Synonyms=Tem7;
Mus musculus (Mouse).
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EMBL, AF378760, AAL11997.1; -.

MGD, MGI-1919574; Plxdc1.

GO, GO:0016020, C:membrane; IEA.

GO, GO:0004872; F:receptor activity; IEA.

GO, GO:000755; Piedevalopment; IEA.

InterPro; IPR00310; IG-11ke.

InterPro; IPR003659; Plexin-like.

InterPro; IPR002165; Plexin-repeat.
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nes 97; Conservative
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SMART; SM00423; PSI; 1
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Matches 97; Conserv
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TISSUE=Ovary
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                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=C57BL/G17 IISSUB=Cerebellum;
MEDLINE=C57BL/G17 IISSUB=Cerebellum;
MEDLINE=C97BL/G409374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 16 days neonate cerebellum CDNA, RIKEN full-length
enriched library, clone:96300400L07 product:TUMOR ENDOTHELIAL MARKER
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STRAIN=C57BL/6J; TISSUB=Cerebellum;
MEDLINE=2530913; PubMed=11076861;
MEDLINE=2530913; PubMed=11076861;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamanoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Cogawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1557-171(2000).
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STRAIN=CS7BL/6J; TISSUE=Cerebellum;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDIANE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                            NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106
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MEDLINE=99279253; PubMed=10349636;
Carninol P., Hayashizaki Yi.
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; IISSUE=Cerebellum;
The FANTOM Consortium,
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Controlling F.S., Wagner L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Strausberg R.L., Seingold E.A., Grouse L.H., Schaefer C.P., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
A Brothero M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broback S.A., WcEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
A Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
A Generation and initial analysis of more than 15,000 full-length human
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Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hiraoka T., Hiraoka T., Hiraoka T., Hiraoka T., Hiraoka T., Hiraoka T., Hiraoka T., Hiraoka T., Hiraoka T., Hiraoka T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S. Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Sasitoh H., Saitoh H., Sakai C., Sakai K., Sakarume N., Sano H., Tagawa A., Takahsahi F., Takaku-Akahira S., Takeda Y., Tanaka T., Towaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; EMBL, AK036144; BAC29318.1;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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SMART; SM00423; PSI; 1.
SEQUENCE 507 AA; 56332 WW; C2D50B44561C3415 CRC64;
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c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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90, G0:0016620; Cimembrane; IBA.

G0; G0:0004872; F:receptor activity; IBA.

G0; G0:0007275; P:development; IBA.
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InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
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01-DEC-2001 (TrEMBLrel. 19,
01-JUN-2003 (TrEMBLrel. 24,
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Conservative
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221 NGTALVVQWDHVHLQDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQ 268
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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TISSUB=Ovary;
Straubaerg R.;
Submitted (40G-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC012885; AAH12885.1; -.
EGG; GO:0016020; C:membrane; IEA.
GO; GO:000472; F:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
                                                                                                                      InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
Pfam; PR01437; PS1; 1.
SEQUENCE : $800423; PS1; 1.
SEQUENCE : $480 AA, 53912 MW; F8DB0E2631BC7816 CRC64;
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                         529 AA
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Genome Res. 13:226.2270(2003).
EMBL; A758446; AAQ88850.1; -.
Interpro; IPR003659; Plexin-like.
Interpro; IPR002165; Plexin_repeat.
Pfam; PP01437; PSI; 1.
SWART; SM00423; PSI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORFNames=UNQ2514;
Homo sapiens (Human).
                                                                                                                                                                                                                              Local Similarity
nes 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
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                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q6UX71;
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Q6UX71
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161 LSFDFPFYGHFLREITVATGGFIYTGEVVHRMLTATQYIAPLMANFDPSVSRNSTVRYFD 220
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                                                                                                                                                                                                                                                           MEDLINE=21443268; PubMed=11559528;
Carson-Walter B.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor endothelial marker 7-related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            221 NGTALVVQWDHVHLQDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQ 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.9%; Score 417; DB 2; Length 529; 72.2%; Pred. No. 1.5e-35; Live 12; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             529 AA; 59583 MW; D44A0975DF894840 CRC64;
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Mammalia; Butheria; Primata; Catarrhini; Hominidae;
01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Tumor endothelial marker 7-related precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Genew; HGNC:21013; PLXDC2.
Go; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR0031659; Plexin_like.
InterPro; IPR002165; Plexin_repeat.
Fan; PF01437; PSI; 1.
SWART; SM00423; PSI; 1.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                     Query Match
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S.W. Worley K.C., Hale S., Garcia A.M., Gab L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ryzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                          1 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                       (SPDI), a Large-Scale
Transmembrane Proteins: A
                                                                                                                                                                 Gaps
Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D. Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P.;
                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22341132; PubMed=12454917;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
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                                                                                                                                                                                                                                                               61 NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
                                                                                                                                      Length 529;
                                                                                                                                                                18; Indels
                                      "The Secreted Protein Discovery Initiative (SPDI), a Li
Effort to Identify Novel Human Secreted and Transmembri
Bioinformatics Assessment.";
Bioinformatics 2265-2270(203).
EMBL, AY358486; AAQ88850.1; -.
SEQUENCE 529 AA; 59583 MW; CCE911D6DF837B40 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2004 (TrEMBLrel. 28, Last sequence update) 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                     70.9%; Score 417; DB 2; 72.2%; Pred. No. 1.5e-35; ive 12; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                              513 AA
                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2004 (TrEMBLrel. 28, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopodinae; Xenopus.
                                                                                                                                                Local Similarity
les 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           initiative.
                                                                                                                                      Query Match
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STRAIN-MRK; TISSUE-Mammary tumor. WAP-Tag model. 5 months old;

X STRAIN-MRK; TISSUE-Mammary tumor. WAP-Tag model. 5 months old;

X Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Klauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

X Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hshelf F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yullalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Nordski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human

"T and mouse CDNA sequences.",
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                                                                                                                                                                                                                                                                                                                146 LSFDFPFYGHFLREITVATGGFIYTGEVVHRMLTATQYIAPLMANFDPSVSRNSTVRYFD 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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STRAIN=NWRI, TISSUE=Mammary tumor. WAP-Tag model. 5 months old;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                  61 NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSV 106
                                                                                                                                    Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 NGTALVVQWDHVHLRDNYSLGSFTFQATLINDGRIVFGYKDIPVPV 251
                                                                                                                                        70.2%; Score 413; DB 2; Length 51
72.6%; Pred. No. 3.8e-35;
tive 12; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Indels
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Strain-bard.
Strain-bard.
Strain-bard.
Strain-bard.
Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, BCG57881, AAH57881.1; --
InterPro; IPR003165; Plexin_repeat.
Pfam; PF01437; PSI; 1.
SMART; SM00423; PSI; 1.
SEQUENCE 530 AA; 59646 MW; D7256C02073417FC CRC64;
EMBL; BC077242; AAH77242.1; -.
Hypothetical protein.
SEQUENCE 513 AA; 57622 MW; 301EA53F2905A4ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        530 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequ
05-JUL-2004 (TrEMBLrel. 27, Last and
17mor endothelial marker 7-related,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                       Best Local Similarity 72.68
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Best Local Similarity
Total 76; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxID=10090;
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SEQUENCE
                                                                                                                                                                                                                                                                                                Query Match
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161 LSFDFPFYGHFLNEVTVATGGFIYTGEVVHRMLTATQYIAPLMANFDPSVSRNSTVRYFD 220
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C STRAIN=C57BL/6J; TISSUB=Lung;

X MEDLINE=205:0913; Pubmed=11076861;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibata K., Itoh M., Aizawa K., Kiteunai T., Tashiro H., Itoh M.,

Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Rujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

A Pujiwake S., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUB=Lung; STRAIN=C57BL/6J; TISSUB=Lung; STRAIN=C57BL/6J; TISSUB=Lung; STRAIN=C57BL/6J; TISSUB=Lung; Strainci E., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; propare full-length cDNA ibraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last amoutation update)
Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
clone:1200007L24 product:TUMOR ENDOTHELIAL MARKER 7-RELATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CSTBL/60; TISSUE-Lung;
Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=21085660; PubMed=11217851;
MIKEN FANTOM CONSOrtium;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                         NGTVFVVQWDHVYLQGWEDKGSFTFQAALHHDGRIVFAYKEIPMSVPE 108
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Lung;
MEDLINE=99279253; PubMed=10349636;
METAINCE, P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Lung;
The FANTOM CONSOITIUM,
                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                        Name=Plxdc2;
                           61
                                                                                                                                                                                                                           homolog.
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Kawai J., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T., Owa C., Salico H., Saito R., Sakai C., Sakai K., Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
Submitted (UUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 LSFDFPFYGHPLRQITIATGGFIFMGDVIHRMLTATQYVAPLMANFNPGYSDNSTVVYFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Carson-Walter B.B., Watkins D.N., Nanda A., Vogelstein B.,
Kinzler K.W., St Croix B.;
"Cell surface tumor endothelial markers are conserved in mice and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Potential.
tumor endothelial marker 7-related.
FF8315020735E36D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 NGTALVVQWDHVHLQDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQ 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.9%; Score 411; DB 2; Length 530; ilarity 70.4%; Pred. No. 6.4e-35; Conservative 13; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                   MOD; MOT:1914698; DIXGC2.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0014872; F:receptor activity; IEA.
GO; GO:0007275; F:development; IEA.
InterPro; IPR008947; PLC Nuclease.
InterPro; IPR008959; Plexin-like.
InterPro; IPR00156; Plexin_repeat.
Pfam; PF01477; PSI; 1.
SMART; SM00422; PSI; 1.
SMART; SM00422; PSI; 1.
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EMBL; AF378761; AAL11998.1; -.
MGD; MGI:1914698; Plxdc2.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000755; P:redevelopment; IEA.
InterPro; IPR003659; Plexin-like.
InterPro; IPR002165; Plexin_repeat.
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01-DEC-2001 (TrEMBLrel. 19, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Plxdc2; Synonyms=Tem7R;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01437; PSI; 1.
SMART; SM00423; PSI; 1.
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530 AA;
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Les 76; Conserv
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Best Local Similarity
Matches 76; Conserv
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